


```
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/671,658A
; FILING DATE: 27-Sep-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-671-658A-2

Query Match          99.6%; Score 1554; DB 5; Length 316;
Best Local Similarity 99.7%; Pred. No. 7.9e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGPLHPAPAPAPAPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLHPAPAPAPAPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 82

QY 61 DSTHCFYRLRLHFNADLQDSTLESEDTLPDSCRMRKQAFQGAQVQKELQHIYGPQRFSGA 120
    |||||||
Db 83 DSTHCFYRLRLHFNAGLQDSTLESEDTLPDSCRMRKQAFQGAQVQKELQHIYGPQRFSGA 142

QY 121 PAMMGSLDVAQQRKPPAPQFAHLTTINAASIPSGSHKVTLSWYHGRGMKISNMTLSN 180
    |||||||
Db 143 PAMMGSLDVAQQRKPPAPQFAHLTTINAASIPSGSHKVTLSWYHGRGMKISNMTLSN 202

QY 181 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMVYVVKTSIKIPSSHNLKMGSGSTKN 240
    |||||||
Db 203 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMVYVVKTSIKIPSSHNLKMGSGSTKN 262

QY 241 WSGNSEFFHYSINVGGFKRLRAGEEISIQVSNPILDPDQATYFGARFYVDID 294
    |||||||
Db 263 WSGNSEFFHYSINVGGFKRLRAGEEISIQVSNPILDPDQATYFGARFYVDID 316

RESULT 3
US-10-105-057-2
; Sequence 2, Application US/10105057
; GENERAL INFORMATION:
; APPLICANT: Barnes-Jewish Hospital, d/b/a The Jewish Hospital of St. Louis
```

```
; TITLE OF INVENTION: STIMULATION OF OSTEOGENESIS USING RANK LIGAND FUSION PROTEINS
; FILE REFERENCE: BICH 10054.1
; CURRENT APPLICATION NUMBER: US/10/105,057
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/277,855
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-105-057-2

Query Match          99.6%; Score 1554; DB 6; Length 316;
Best Local Similarity 99.7%; Pred. No. 7.9e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 82

QY 61 DSTHCFYRLRLHFNADLQDSTLESEDTLPDSCRMRKQAFQGAQVQKELQHIYGPQRFSGA 120
    |||||||
Db 83 DSTHCFYRLRLHFNAGLQDSTLESEDTLPDSCRMRKQAFQGAQVQKELQHIYGPQRFSGA 142

QY 121 PAMMGSLDVAQQRKPPAPQFAHLTTINAASIPSGSHKVTLSWYHGRGMKISNMTLSN 180
    |||||||
Db 143 PAMMGSLDVAQQRKPPAPQFAHLTTINAASIPSGSHKVTLSWYHGRGMKISNMTLSN 202

QY 181 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMVYVVKTSIKIPSSHNLKMGSGSTKN 240
    |||||||
Db 203 GKLRYNODGFYLLYANICFRHHTSGSVPTDYLDLMVYVVKTSIKIPSSHNLKMGSGSTKN 262

QY 241 WSGNSEFFHYSINVGGFKRLRAGEEISIQVSNPILDPDQATYFGARFYVDID 294
    |||||||
Db 263 WSGNSEFFHYSINVGGFKRLRAGEEISIQVSNPILDPDQATYFGARFYVDID 316

RESULT 4
PCT-US02-16002-10
; Sequence 10, Application PC/TUS0216002
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-WO
; CURRENT APPLICATION NUMBER: PCT/US02/16002
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16002-10

Query Match          85.0%; Score 1326.5; DB 1; Length 317;
Best Local Similarity 84.5%; Pred. No. 2.2e-111;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 1 GVPHEGPLHPAPAPAPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 60
    |||||||
Db 23 GVPHEGPLH-APPPAPQPPAASRSMFLALLGLGLGVVCSIALFLYFRAQMPNRISE 81

QY 61 DSTHCFYRLRLHFNADLQDSTLESEDT--LPDSCRMRKQAFQGAQVQKELQHIYGPQRFSGA 118
    |||||||
Db 82 DSTHCFYRLRLHFNADFDQDTLESQDTKLIPDSCRMRKQAFQGAQVQKELQHIYGSQHIR 141
```

```
OY 119 GAPAMGSSWLDVAORGKPEAOPFAHLITINAAIPSGSHKVTLSWYHNRGMAKISNMTL 178
      ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:|
Db 142 AEKAWDGSWLDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHNRGMAKISNMTF 201
OY 179 SNGKLRVNODGFYLYLANICFRHHETSGSVPTDYQLMWYVVKTSIKIPSSHNLKKGST 238
      ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:|
Db 202 SNGKLRVNODGFYLYLANICFRHHETSGDLATEYLQLMVYVVKTSIKIPSSHNLKKGST 261
OY 239 KMWGNSSEHFHSINVGCFKLRAGEEISIOVNSPLDDPDODATYFGAFYQDID 294
      | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 262 KMWGNSSEHFHSINVGCFKLRAGEEISIEVNSPLDDPDODATYFGAFYQDID 317

RESULT 5
US-10-151-071-10
; Sequence 10, Application US/10151071
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William
; APPLICANT: ANDERSON, DITR
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-10

Query Match 85.0%; Score 1326.5; DB 6; Length 317;
Best Local Similarity 84.5%; Pred. No. 2.2e-111;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

OY 1 GVNHEGRLHPAPAPAPAPAPASRSMFLALGLGQVCSIALFLYFRAMDNRRISE 60
      | |||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:|
Db 23 GAPHEGRLH-APPAPAPAPAPAPASRSMFLALGLGQVCSIALFLYFRAMDNRRISE 81
OY 61 DSTHCFYRLRHEHNAADIDSTLESDT--LPDSCRMRKQAFQAVQKELQIHVGPQRS 118
      | |||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:|
Db 82 DCTHCTYRLRHEHNAADIDSTLESDT--LPDSCRMRKQAFQAVQKELQIHVGPQRS 141
OY 119 GAPAMGSSWLDVAORGKPEAOPFAHLITINAAIPSGSHKVTLSWYHNRGMAKISNMTL 178
      ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:| ||:|||||:|:|
Db 142 AEKAWDGSWLDLAKRSKLEAOPFAHLITINATDIPSGSHKVSLSWYHNRGMAKISNMTF 201
OY 179 SNGKLRVNODGFYLYLANICFRHHETSGSVPTDYQLMWYVVKTSIKIPSSHNLKKGST 238
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 202 SNGKLRVNODGFYLYLANICFRHHETSGDLATEYLQLMVYVVKTSIKIPSSHNLKKGST 261
OY 239 KMWGNSSEHFHSINVGCFKLRAGEEISIOVNSPLDDPDODATYFGAFYQDID 294
      | |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 262 KMWGNSSEHFHSINVGCFKLRAGEEISIEVNSPLDDPDODATYFGAFYQDID 317

RESULT 6
PCT-US02-16106-41
; Sequence 41, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: P5554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-16106-41

Query Match 16.6%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.9e-15;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRSMFLALGLGQVCSIALFLYFRAMD--PNRISDSYHCFYRLRHEHNDL 78
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 10 PSLGQTCVLIYFVLLQSLCAVATYVYFETNELKQMQKYSKSGIACF-----LKEDSY 64
OY 79 QDSTLESFDTLPDSCRMRKQAFQAVQK-----ELQHYGPORFSGAPAMM 124
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 65 WDP--NDEESMNSPCMQYKWLRLVKKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAORGKPEAOPFAHLT-----INAAIPSGSHKVTL---SSWYHDR-GMAKIS 174
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 114 -----VERGQRYA--AHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NKTLSNGKLRVNODGFYLYLANICFRHHETSGSVPTDYQLMWYVVKTSIKIPSSHNLK 234
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 166 NLHRLNGELVHIEKGFYIYQTYRFOEIKENTKNDKQWQYLYKYT-SYPPDILMK 224
OY 235 GSGTSMGNSSEHFHSINVGCFKLRAGEEISIOVNSPLDDPDODATYFGAFY 290
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 225 SARNSCKSDAEYGLSYQGIPELKENDRIFVSVTNEHLIDMDEASFGAFY 280

RESULT 7
US-10-039-785-66
; Sequence 66, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunologically Bind to TRAIL
; FILE REFERENCE: P5550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 16.6%; Score 258.5; DB 6; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.9e-15;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
```


Tue Jul 9 13:21:01 2002

us-09-865-363-11.rapn

Page 7

Db 215 NSKYPQDLVME-GKMSYCTTGOMMARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ 273
Oy 283 TYFGAFKV 290
Db 274 TFFGLYKL 281

Search completed: July 8, 2002, 19:54:09.
Job time: 12488 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:06:01 ; Search time 4715.96 Seconds

(without alignments)
7232.940 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630
Sequence: 1 CCGCGCTCCACAGAGCGT.....TAACCTAATAGAGCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GeneB1: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_higo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	1630	100.0	1630	6	AR156433	AR156433 Sequence
2	1630	100.0	1630	6	AR164147	AR164147 Sequence
3	1630	100.0	1630	6	AX147987	AX147987 Sequence
4	1630	100.0	2225	10	AF019048	AF019048 Mus muscu
5	1628.4	99.9	2295	6	AR062119	AR062119 Sequence
6	1628.4	99.9	2299	10	AF053713	AF053713 Mus muscu
7	1615.8	99.1	2191	6	AR157058	AR157058 Sequence
8	1615.8	99.1	2191	6	AX140162	AX140162 Sequence
9	1588.2	97.4	2237	10	AF013170	AF013170 Mus muscu
10	1152.4	70.7	2029	6	E34349	E34349 DNA and pro
11	1152.4	70.7	2029	10	AB022036S4	AB022039 Mus muscu
12	939.6	57.6	2271	9	AF053712	AF053712 Homo sapl
13	928.6	57.0	2201	9	AF019047	AF019047 Homo sapl
14	885.4	54.3	951	6	E34350	E34350 DNA and pro
15	885.4	54.3	951	6	E34388	E34388 Novel prote
16	885.4	54.3	951	10	AB008426	AB008426 Mus muscu
17	885.4	54.3	951	10	AB036798	AB036798 Mus muscu
18	843.2	51.7	2390	6	AX201362	AX201362 Sequence
19	832.8	51.1	1823	9	AF013171	AF013171 Homo sapl
20	816.6	50.1	864	10	AB032771	AB032771 Homo sapl
21	773.4	47.4	957	10	AF187319	AF187319 Mus muscu
22	724.4	44.4	754	10	AB032772	AB032772 Mus muscu
23	653.6	40.1	113451	2	AC032327	AC032327 Homo sapl
24	653.6	40.1	200724	9	AL139382	AL139382 Human DNA
25	618.4	37.9	809	10	AF425669	AF425669 Rattus no
26	615	37.7	954	6	AR156434	AR156434 Sequence
27	615	37.7	954	6	AR164148	AR164148 Sequence
28	615	37.7	954	6	AX147989	AX147989 Sequence
29	615	37.7	1034	9	AB064269	AB064269 Homo sapl
30	588.8	36.1	972	9	AB064270	AB064270 Homo sapl
31	584.2	35.8	911	9	AB061227	AB061227 Homo sapl
32	556.8	34.2	818	9	AB064268	AB064268 Homo sapl
33	547.4	33.6	930	9	AB037599	AB037599 Homo sapl
34	475.2	29.2	123551	2	AC094149	AC094149 Rattus no
35	466	28.6	522	6	AX232589	AX232589 Sequence
36	165.8	10.2	468	6	E34347	E34347 DNA and pro
37	165.8	10.2	468	10	AB022036S2	AB022037 Mus muscu
38	159.4	9.8	764	10	AB022036S1	AB022036 Mus muscu
39	157.8	9.7	2026	6	E34346	E34346 DNA and pro
40	130	8.0	123551	2	AC094149	AC094149 Rattus no
41	105.8	6.5	575	6	E34348	E34348 DNA and pro
42	105.8	6.5	575	10	AB022036S3	AB022038 Mus muscu
43	97	6.0	161835	2	AC104794	AC104794 Homo sapl
44	97	6.0	190748	9	AC010969	AC010969 Homo sapl
45	91.4	5.6	2460	5	AF250041	AF250041 Danio rer

ALIGNMENTS

RESULT 1	AR156433	1630 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR156433				
DEFINITION	Sequence 10 from patent US 6242213.				
ACCESSION	AR156433				
VERSION	AR156433.1	GI:15125137			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1630)				
AUTHORS	Anderson,D.M.				
TITLE	Isolated DNA molecules encoding RANK-L				
JOURNAL	Patent: US 6242213-A 10 05-JUN-2001;				
FEATURES	Location/Qualifiers				
source	1..1630				
BASE COUNT	436 a 355 c 379 g 460 t				
ORIGIN					

Query Match	100.0%	Score 1630;	DB 6;	Length 1630;
Best Local Similarity	100.0%;	Pred. No. 0;		

Matches	1630;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	CCGGCGTCCACAGAGAGTCCGCTGCACCCCGGCTTCTGCACCGGCTCCGGCCGC							60
Db	1	CCGGCGTCCACAGAGAGTCCGCTGCACCCCGGCTTCTGCACCGGCTCCGGCCGC							60
QY	61	CACCCGCCGCTCCCGCTCCATGTTCTGCGCCCTCGGGGCTGGGAGCTGGGAGCTGG							120
Db	61	CACCCGCCGCTCCCGCTCCATGTTCTGCGCCCTCGGGGCTGGGAGCTGGGAGCTGG							120
QY	121	TCCTCAGCATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							180
Db	121	TCCTCAGCATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							180
QY	181	AAGACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							240
Db	181	AAGACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							240
QY	241	ACTGAGCTGAG							300
Db	241	ACTGAGCTGAG							300
QY	301	TTGAGGGGCGGCTGAG							360
Db	301	TTGAGGGGCGGCTGAG							360
QY	361	CTCAGCTATGATGAG							420
Db	361	CTCAGCTATGATGAG							420
QY	421	AGCCATTTGCACACCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							480
Db	421	AGCCATTTGCACACCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							480
QY	481	CTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							540
Db	481	CTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							540
QY	541	ACGGAATCTAAGGTTAAACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							600
Db	541	ACGGAATCTAAGGTTAAACCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							600
QY	601	GACATCATGAACATCGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							660
Db	601	GACATCATGAACATCGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							660
QY	661	TTAAACCAAGCATCAAAATCCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							720
Db	661	TTAAACCAAGCATCAAAATCCCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							720
QY	721	ACTGCTGGGCAATCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG							780
Db	721	ACTGCTGGGCAATCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG							780
QY	781	TCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							840
Db	781	TCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							840
QY	841	AAGATGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							900
Db	841	AAGATGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							900
QY	901	GAAACATTAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							960
Db	901	GAAACATTAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							960
QY	961	ACATGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1020
Db	961	ACATGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1020
QY	1021	TTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1080
Db	1021	TTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1080

QY	1081	TACACAGGTTTACATTTTGAATGATTTCTAGAAATGGAACCAAGATTGGAGAGGT							1140
Db	1081	TACACAGGTTTACATTTTGAATGATTTCTAGAAATGGAACCAAGATTGGAGAGGT							1140
QY	1141	ATTCCAGTCTTATGAAAACCTTACAGCTGAGCTATGGAAGGGGCTCACAGTCTGGGT							1200
Db	1141	ATTCCAGTCTTATGAAAACCTTACAGCTGAGCTATGGAAGGGGCTCACAGTCTGGGT							1200
QY	1201	CTAACCCCTGGACATGCGCACAGTAAGCTGGAATTAAGAGATGCCATGTCATGCA							1260
Db	1201	CTAACCCCTGGACATGCGCACAGTAAGCTGGAATTAAGAGATGCCATGTCATGCA							1260
QY	1261	AAGAAATGATGCTGAGAGAGGTTAAGTTCTTTGAAATGTTTACATGCGCTGGAGCTGC							1320
Db	1261	AAGAAATGATGCTGAGAGAGGTTAAGTTCTTTGAAATGTTTACATGCGCTGGAGCTGC							1320
QY	1321	AAATAGTCTCTTTTCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG							1380
Db	1321	AAATAGTCTCTTTTCTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG							1380
QY	1381	AAGTATATTTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG							1440
Db	1381	AAGTATATTTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG							1440
QY	1441	AGTATTTGATTCAAATATTTTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1500
Db	1441	AGTATTTGATTCAAATATTTTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1500
QY	1501	TACAGATGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1560
Db	1501	TACAGATGATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT							1560
QY	1561	GCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							1620
Db	1561	GCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							1620
QY	1621	GAGTCTTCAG 1630							
Db	1621	GAGTCTTCAG 1630							
RESULT	2								
AR164147	AR164147	1630 bp	DNA	linear	PAT 17-OCT-2001				
LOCUS	Sequence 10 from patent US 6271349.								
DEFINITION	AR164147								
ACCESSION	AR164147								
KEYWORDS	AR164147.1 GI:16235112								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 1630)								
AUTHORS	Dougall, W.C. and Galibert, L.								
TITLE	Receptor activator of NF- κ B								
JOURNAL	Patent: US 6271349-A 10 07-AUG-2001;								
FEATURES	Location/Qualifiers								
source	1..1630								
BASE COUNT	436 a 355 c 379 g 460 t								
ORIGIN									
Query Match	100.0%; Score 1630; DB 6; Length 1630;								
Best Local Similarity	100.0%; Pred. No. 0;								
Matches 1630; Conservative	0; Mismatches 0; Indels 0; Gaps 0;								
QY	1	CCGGCGTCCACAGAGAGTCCGCTGCACCCCGGCTTCTGCACCGGCTCCGGCCGC							60
Db	1	CCGGCGTCCACAGAGAGTCCGCTGCACCCCGGCTTCTGCACCGGCTCCGGCCGC							60
QY	61	CACCCGCCGCTCCCGCTCCATGTTCTGCGCCCTCGGGGCTGGGAGCTGGGAGCTGG							120
Db	61	CACCCGCCGCTCCCGCTCCATGTTCTGCGCCCTCGGGGCTGGGAGCTGGGAGCTGG							120

Dh 61 CACCCGCCCTCCGCTCCATGTTCTTGCCCTCTTGCGGCGCTGGGACTGGCCAGGTGG 120
Qy 121 TCTGAGAGATCGCTGTTCTGTTCTGTTCTGAGCGCAGATGGATCTTAACAGATATCAG 180
Dh 121 TCTGAGAGATCGCTGTTCTGTTCTGTTCTGAGCGCAGATGGATCTTAACAGATATCAG 180
Qy 181 AAGACAGACACTGCTGTTTATAGAAATCTGAGACTCCATGMAAACGACAGATTTGACG 240
Dh 181 AAGACAGACACTGCTGTTTATAGAAATCTGAGACTCCATGMAAACGACAGATTTGACG 240
Qy 241 ACTGACCTGAGAGATGAAGACACATACCTGACTCTGCGAGAGAGATGAAGAACGCT 300
Dh 241 ACTGACCTGAGAGATGAAGACACATACCTGACTCTGCGAGAGAGATGAAGAACGCT 300
Qy 301 TTCCAGGGGGCCGTGAGAGAGAACTCAACATTTGGGGCCACAGGCTTCTCAGAG 360
Dh 301 TTCCAGGGGGCCGTGAGAGAGAACTCAACATTTGGGGCCACAGGCTTCTCAGAG 360
Qy 361 CTCACGCTATGATGAGAGGCTCATGTTGGATGTGGCCAGCGAGCAAGCTGAGGGCC 420
Dh 361 CTCACGCTATGATGAGAGGCTCATGTTGGATGTGGCCAGCGAGCAAGCTGAGGGCC 420
Qy 421 AGCCATTTGACACCTCAACATCATGCTGCGACATCCCATCGGGTTCCCATTAAGTCA 480
Dh 421 AGCCATTTGACACCTCAACATCATGCTGCGACATCCCATCGGGTTCCCATTAAGTCA 480
Qy 481 CTCTGCTCTTGTGATACACGATCGAGGCTGGCCAAAGATCTTAACATGAGCTTAAGCA 540
Dh 481 CTCTGCTCTTGTGATACACGATCGAGGCTGGCCAAAGATCTTAACATGAGCTTAAGCA 540
Qy 541 ACGGAAACCTAAGGTTAACCAAGATGCTTATTTACCTGTGACCAACATTTGCTTTC 600
Dh 541 ACGGAAACCTAAGGTTAACCAAGATGCTTATTTACCTGTGACCAACATTTGCTTTC 600
Qy 601 GGCATCATGAAGAACTGGGAGGCTACCTACAGACTATCTTCAAGTGTGATGTGCG 660
Dh 601 GGCATCATGAAGAACTGGGAGGCTACCTACAGACTATCTTCAAGTGTGATGTGCG 660
Qy 661 TTAAAAACAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGAGCAAGAAA 720
Dh 661 TTAAAAACAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGAGCAAGAAA 720
Qy 721 ACTGTCGGGGCAATTTCTCAATTTCCATTTTATTCATTAATGTTGGGGGATTTTCAAGC 780
Dh 721 ACTGTCGGGGCAATTTCTCAATTTCCATTTTATTCATTAATGTTGGGGGATTTTCAAGC 780
Qy 781 TCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGCCAACCCCTTCCCTGATCCGGATC 840
Dh 781 TCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGCCAACCCCTTCCCTGATCCGGATC 840
Qy 841 AAGATCGCAGCTACTTGTGGGCTTTCAAGTTCAGAGCATGAGACTCATTTCTGCTG 900
Dh 841 AAGATCGCAGCTACTTGTGGGCTTTCAAGTTCAGAGCATGAGACTCATTTCTGCTG 900
Qy 901 GAACATTTGCAATGATGCTCTAGATGTTTGAAGCTTCTTAAGAAATGATGATGCTAT 960
Dh 901 GAACATTTGCAATGATGCTCTAGATGTTTGAAGCTTCTTAAGAAATGATGATGCTAT 960
Qy 961 ACATGTGTAAGACTACTTAAGAGACATGGCCAGGCTGATGAAGCTCAGACCCCTCTC 1020
Dh 961 ACATGTGTAAGACTACTTAAGAGACATGGCCAGGCTGATGAAGCTCAGACCCCTCTC 1020
Qy 1021 TTGAGCCTGTACAGGTTGTATATGTAAGTCCATAGCTGATGTTAGATCATGATGAT 1080
Dh 1021 TTGAGCCTGTACAGGTTGTATATGTAAGTCCATAGCTGATGTTAGATCATGATGAT 1080
Qy 1081 TACACAAACGTTTATCAATTTTGTATATGATTTCTAGATTTGAACACAGATTGGAGAGCT 1140
Dh 1081 TACACAAACGTTTATCAATTTTGTATATGATTTCTAGATTTGAACACAGATTGGAGAGCT 1140
Qy 1141 ATTCCGATCTTATGAAGAAACCTTACAGCTGAGCTATGGAAGGGGCTCAGACTCTGGGT 1200
Dh 1141 ATTCCGATCTTATGAAGAAACCTTACAGCTGAGCTATGGAAGGGGCTCAGACTCTGGGT 1200

Qy 1201 CTAAACCCCTGGACATGTGCGACACTGAGAACCTTGAATTAAGAGATGGCATGTATTGCA 1260
Dh 1201 CTAAACCCCTGGACATGTGCGACACTGAGAACCTTGAATTAAGAGATGGCATGTATTGCA 1260
Qy 1261 AAGAAATGATAGTGAAGGGTTAAGTTCTTTGAAATGTTACATTTGGCTGGGACCTGCG 1320
Dh 1261 AAGAAATGATAGTGAAGGGTTAAGTTCTTTGAAATGTTACATTTGGCTGGGACCTGCG 1320
Qy 1321 AAATPAAGTTCTTTTCTTAAATGAGAGAGAAATATATGATATTTTATTAATGCTCA 1380
Dh 1321 AAATPAAGTTCTTTTCTTAAATGAGAGAGAAATATATGATATTTTATTAATGCTCA 1380
Qy 1381 AAGTATATTTACAGGTGAATGTTTCTGCAAGAGTTTGTAAATTAATTTGTCAT 1440
Dh 1381 AAGTATATTTACAGGTGAATGTTTCTGCAAGAGTTTGTAAATTAATTTGTCAT 1440
Qy 1441 AGTATTTGATTCAAATAATTTAAAAATGTCACGTGTGACATATTAATGTTTAAATG 1500
Dh 1441 AGTATTTGATTCAAATAATTTAAAAATGTCACGTGTGACATATTAATGTTTAAATG 1500
Qy 1501 TACAGATGATTTAACTGCTGCTGCTTGTAAATTTCCCTGAAAGTACGCTAGTAAGGG 1560
Dh 1501 TACAGATGATTTAACTGCTGCTGCTTGTAAATTTCCCTGAAAGTACGCTAGTAAGGG 1560
Qy 1561 GCAGAAATCTGTTCTGCTGACACATGATGATTTATTTCTTATTTTAACTTAAATA 1620
Dh 1561 GCAGAAATCTGTTCTGCTGACACATGATGATTTATTTCTTATTTTAACTTAAATA 1620
Qy 1621 GAGTCTTCAG 1630
Dh 1621 GAGTCTTCAG 1630

RESULT 3
AX147987
LOCUS AX147987 1630 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0136637.
ACCESSION AX147987
VERSION AX147987.1 GI:14346962
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1630)
AUTHORS Anderson,D.M. and Hughes,A.E.
TITLE Receptor activator of nf-kappa b
JOURNAL Patent: WO 0136637-A 10 25-MAY-2001.
Immunex Corporation (US)
FEATURES
source location/Qualifiers
1..1630
/organism="Mus musculus"
/db_xref="taxon:10090"
CDS
3..887
/note="unnamed protein product"
/codon_start=1
/protein_id="CA41184.1"
/db_xref="GI:14346963"
/translation="GVPHGEPHLPAPAPAPAPAPASRSMFLALLGLGLGVCSIA
LFLYFRAMDNPRISEDSHCYFRLRLHFNADLQSTLESEDTLPDSCHRMQAFQ
AVQKLEQHLIVGPFSGAPAPAMEGSMIDVQROKPAOPAPALITINAASIPSGSHKVT
LSWYHNRGMAKISNMTLSNGLRVNDGPLYLYANICPEPHHETSGSPVDTYLOLVY
VVTSTIKPSSHLMMGSGSKRMSNSSEPHFYISINVGFPFKLAGEEISIQVSNPSLL
DPDQDAPTFEAFVQDID"

BASE COUNT 436 a 355 c 379 g 460 t
ORIGIN

Query Match 100.0%; Score 1630; DB 6; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	CCGGCGTCCACACGAGGGTCCGCTGCAACCCCGGCCCTTTCTGCACGGGCTCCGGCGCCG	60
Db	1	CCGGCGTCCACACGAGGGTCCGCTGCAACCCCGGCCCTTTCTGCACGGGCTCCGGCGCCG	60
OY	61	CACCGCGCGCTCCCGCTCCATGTTCTCGGCCCTCTGGGGCTGGGACTGGGGCAGGTG	120
Db	61	CACCGCGCGCTCCCGCTCCATGTTCTCGGCCCTCTGGGGCTGGGACTGGGGCAGGTG	120
OY	121	TCGCAACATGCTCTGTCTCTGTCTTCTTCTGAGCGCAATGGATCTTAACAAATATCAG	180
Db	121	TCGCAACATGCTCTGTCTCTGTCTTCTTCTGAGCGCAATGGATCTTAACAAATATCAG	180
OY	181	AAGACACACTCATCTGCTTTTATAGAACTCTAGACTCTCATGAAACAGACATTTGCAG	240
Db	181	AAGACACACTCATCTGCTTTTATAGAACTCTAGACTCTCATGAAACAGACATTTGCAG	240
OY	241	ACTGCACTCGAGAGTGAAGACACACTACCTGACTCCTGAGAGAGATGAACACGCT	300
Db	241	ACTGCACTCGAGAGAGTGAAGACACACTACCTGACTCCTGAGAGAGATGAACACACCT	300
OY	301	TTTCAGGGGGCGCTGCAAGAGAACTGCAATGTGGGGCCACAGCGCTTCCACAGAG	360
Db	301	TTTCAGGGGGCGCTGCAAGAGAACTGCAATGTGGGGCCACAGCGCTTCCACAGAG	360
OY	361	CTCCAGCTATGATGGAAGGCTCATGCTGTGATGTGGCCAGCGAGGCAAGCCTGAGGCC	420
Db	361	CTCCAGCTATGATGGAAGGCTCATGCTGTGATGTGGCCAGCGAGGCAAGCCTGAGGCC	420
OY	421	AGCCATTGGACACCTCTCCATCATATGCTGCCAGCATCCCATCGGGGTCCCATTAATCA	480
Db	421	AGCCATTGGACACCTCTCCATCATATGCTGCCAGCATCCCATCGGGGTCCCATTAAGCA	480
OY	481	CTCTGCTCTTGGTATACACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGCA	540
Db	481	CTCTGCTCTTGGTATACACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGCA	540
OY	541	ACGAAAACCTAAGGGTTAACCAAGATGCGTCTATTTACTGTACCCAACTTTGCTTTC	600
Db	541	ACGAAAACCTAAGGGTTAACCAAGATGCGTCTATTTACTGTACCCAACTTTGCTTTC	600
OY	601	GGCATCATGAAACATCGGGAAGGCTACACAGACTCTTACGTGATGCTGATGTCG	660
Db	601	GGCATCATGAAACATCGGGAAGGCTACCTACAGACATCTTAGCTGATGCTGATGTCG	660
OY	661	TTAAACACGACATCAAAATCCCAAGTCTCATACCTGATGAAGAGAGGAGACAGAAA	720
Db	661	TTAAACACGACATCAAAATCCCAAGTCTCATACCTGATGAAGAGAGAGGAGACAGAAA	720
OY	721	ACTGCTGGGAATTCGAAATTCACCTTATTTCCATAAGTTGGGGATTTTTCAAAC	780
Db	721	ACTGCTGGGAATTCGAAATTCACCTTATTTCCATAAATTTTGGGGATTTTTCAAAC	780
OY	781	TCGCGAGTGTGAAGAAATTAGCATTCAGGTGTCAACCCCTCCCTGCTGATCOGATC	840
Db	781	TCGCGAGTGTGAAGAAATTAGCATTCAGGTGTCAACCCCTCCCTGCTGATCOGATC	840
OY	841	AAGATGCACTACTTTGGGGCTTTCAAAGTTAGAGACATACTGAACATCATTTGCTG	900
Db	841	AAGATGCACTACTTTGGGGCTTTCAAAGTTAGAGACATACTGAACATCATATTGCTG	900
OY	901	GAACATTGTGATGATGATCTCTAGATGTTTGGAACTCTTAAAAAATGGATGATGTCAT	960
Db	901	GAACATTGTGATGATGATCTCTAGATGTTTGGAACTCTTAAAAAATGATGATGTCAT	960
OY	961	ACATGTGTAACTACTPAAGAGACATGGCCACGTTGATGAACCTCACAGCCCTCTCTC	1020
Db	961	ACATGTGTAACTACTPAAGAGACATGGCCACGTTGATGAACCTCACAGCCCTCTCTC	1020
OY	1021	TTGAGCCGTGACAGTTGTGTATATGTAAGTCCATAGGTGATGTTAGTTATGTCGAT	1080
Db	1021	TTGAGCCGTGACAGTTGTGTATATGTAAGTCCATAGGTGATGTTAGTTATGTCGAT	1080
OY	1081	TACACACAGGTTTACATTTTGTAAATGATTTCTGTGAATTAACACAGATTTGGAGAGGT	1140

Db	1081	TACACAAGGCTTTTTCATATTTTGTATATATTTCCTAGAATTGAACACAGATTGGGAGAGT	1140
Qy	1141	ATTCCGATGCTTATGAAAAAATTACACGTGACCTATGSAAGGGGTGCAGTCTTGGGT	1200
Db	1141	ATTCGATGCTTATGAAAAAATTACACGTGACCTATGSAAGGGGTGCAGTCTTGGGT	1200
Qy	1201	CTAACCCCGGACATGTGCGACACTGAGAACCTTGAATTAAGAGATGCCATGCTATTTGCA	1260
Db	1201	CTAACCCCGGACATGTGCGACACTGAGAACCTTGAATTAAGAGATGCCATGCTATTTGCA	1260
Qy	1261	AAGAAATGATGACTGTGAAGGGTTAAGCTTTTGAATTTACATTGCGCTGGACCTGC	1320
Db	1261	AAGAAATGATGACTGTGAAGGGTTAAGCTTTTGAATTTACATTGCGCTGGACCTGC	1320
Qy	1321	AAATAAGTCTTTTCTTCTTAATGAGAGAGAAAAATATGATATTTATATATAGTCTTA	1380
Db	1321	AAATAAGTCTTTTCTTCTTAATGAGAGAGAAAAATATGATATTTATATATAGTCTTA	1380
Qy	1381	AAATTAATATTCAGGTGTAATGTTTCTGTGCAAGTTTGTAAATTAATTTGTGCTAT	1440
Db	1381	AAATTAATATTCAGGTGTAATGTTTCTGTGCAAGTTTGTAAATTAATTTGTGCTAT	1440
Qy	1441	ACTATTATGATTTAAATATTTTAAAAATGTCACACTGTGACATATTTAATGTTTAAATG	1500
Db	1441	ACTATTATGATTTAAATATTTTAAAAATGTCACACTGTGACATATTTAATGTTTAAATG	1500
Qy	1501	TACAGATGATTTAACTGCTGTCATTTTGAATTCCTCGAAGAGTACTGTAAGGAGG	1560
Db	1501	TACAGATGATTTAACTGCTGTCATTTTGAATTCCTCGAAGAGTACTGTAAGGAGG	1560
Qy	1561	GCAGATACTGTTTCTGTCGACACATGATTTATTTCTTATCTTTTAACTTAATA	1620
Db	1561	GCAGATACTGTTTCTGTCGACACATGATTTATTTCTTATCTTTTAACTTAATA	1620
Qy	1621	GAGCTCTTCAG	1630
Db	1621	GAGCTCTTCAG	1630
RESULT	4		
AF019048		2225 bp	linear
LOCUS			AF019048
DEFINITION			Mus musculus receptor activator of nuclear factor kappa B ligand
ACCESSION			AF019048
VERSION			AF019048.1
KEYWORDS			GI:2612923
SOURCE			
ORGANISM			house mouse.
			Mus musculus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
			1 (bases 1 to 2225)
REFERENCE			Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
AUTHORS			Tometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
			Galibert,L.
TITLE			A homologue of the TNF receptor and its ligand enhance T-cell
			growth and dendritic-cell function
JOURNAL			Nature 390 (6656), 175-179 (1997)
MEDLINE			98032977
REFERENCE			2 (bases 1 to 2225)
AUTHORS			Cosman,D., Dubose,R. and Galibert,L.
TITLE			Direct Submission
JOURNAL			Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
FEATURES			University St., Seattle, WA 98101, USA
source			Location/Qualifiers
			1..2225
			/organism="Mus musculus"
			/db_xref="taxon:10090"
			1..2225
			/gene="RANKL"
			137..1087
CDS			

/gene="RANKL"
/mole="receptor activator of nuclear factor kappa B
ligand"
/codon_start=1
/product="RANKL"
/protein_id="AA86812.1"
/db_xref="GI:2612924"
/translation="MRAASNDYKYLRSSEEMSGPCVPHGRLHPAPAPAPPA
ASRMPFALLGLIGOVCSIALFLYERAPMDPRISSESTHCFYRLIRHENDLDD
STLESDLPDSCKRMKAFQAVOKELHIVPQRSGA PAMMEGSLDVAORGRE
AOPRAHLITINASTPSSHKVYLLSSMHDGMKATISMTLSNGLRKNOCFTYLYAN
ICFRHETSSGVPTDYLQIMYVVKISIKIPSSHNLMKGSSTKMSNSSEHFSYINV
GGEFKLAGEISLIVQSNPSLLDDPDQATFYGAARKYODID"

BASE COUNT 623 a 468 c 523 g 611 t
ORIGIN

Query Match 100.0%; Score 1630; DB 10; Length 2225;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCGGCGTCCACAGAGGGTCCGCGCACCCGCGCTTTCACACGGCTCCGGGCGCCG 60
|||||
Db 201 CCGGCGTCCACAGAGGGTCCGCGCACCCGCGCTTTCACACGGCTCCGGGCGCCG 260
61 CACCCGCGCTCCGCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
|||||
Db 261 CACCCGCGCTCCGCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 320
121 TCTGAGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
|||||
Db 321 TCTGAGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 380
181 AAGACGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
|||||
Db 381 AAGACGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 440
241 ACTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
|||||
Db 441 ACTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 500
301 TTCAGGGGCGCGTGCAGAGGACGCAACATTTGGGGGCGCACAGCGCTTTCAGAG 360
|||||
Db 501 TTCAGGGGCGCGTGCAGAGGACGCAACATTTGGGGGCGCACAGCGCTTTCAGAG 560
361 CTCAGCTATGATGGAAGGCTCATGTTGATGTTGGCCACGAGGAGAGGCTGAGGCC 420
|||||
Db 561 CTCAGCTATGATGGAAGGCTCATGTTGATGTTGGCCACGAGGAGAGGCTGAGGCC 620
421 AGCGATTGGACACCTCAATGCTGCGACATCCCATCGGGTTCCTATAAGTCA 480
|||||
Db 621 AGCGATTGGACACCTCAATGCTGCGACATCCCATCGGGTTCCTATAAGTCA 680
481 CTCTGCTCTTGGTACACAGATGAGGCTGGGCGCAAGATCTTAACATGAGCTTAAGCA 540
|||||
Db 681 CTCTGCTCTTGGTACACAGATGAGGCTGGGCGCAAGATCTTAACATGAGCTTAAGCA 740
541 ACGGAAAACCTAAGGCTTAACCAAGTCTTAATACCTGCTACGCCAACATTTGCTTTC 600
|||||
Db 741 ACGGAAAACCTAAGGCTTAACCAAGTCTTAATACCTGCTACGCCAACATTTGCTTTC 800
601 GGCATCATGAACATGGGGAAGCTACCTACAGACTATCTTCACCTGATGCTGATGCTG 660
|||||
Db 801 GGCATCATGAACATGGGGAAGCTACCTACAGACTATCTTCACCTGATGCTGATGCTG 860
661 TTTAAACACAGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGAGCAAGAAA 720
|||||
Db 861 TTTAAACACAGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGGAGCAAGAAA 920
721 ACTGCTGGGGAATTTGGAATTCATCTTTATTCATTAATGTTGGGGGATTTTCAAGC 780
|||||
Db 921 ACTGCTGGGGAATTTGGAATTCATCTTTATTCATTAATGTTGGGGGATTTTCAAGC 980

781 TCCGAGCTGTGAAGAAATATGATTCAGGTGTCCAAACCCCTTCCTGCTGATCCGGATC 840
|||||
Db 981 TCCGAGCTGTGAAGAAATATGATTCAGGTGTCCAAACCCCTTCCTGCTGATCCGGATC 1040
841 AAGATCGGACGTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGACTGACATTTTCGTG 900
|||||
Db 1041 AAGATCGGACGTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGACTGACATTTTCGTG 1100
901 GAACATTAAGCATGATGTCTCCAGATGTTTGAAGAACTTTAAAAATGATGATGCTTAT 960
|||||
Db 1101 GAACATTAAGCATGATGTCTCCAGATGTTTGAAGAACTTTAAAAATGATGATGCTTAT 1160
961 ACATGTGAAGACACTAAGAGACATGAGCCACGCGTGTATGAACCTACAGCCCTCTCTC 1020
|||||
Db 1161 ACATGTGAAGACACTAAGAGACATGAGCCACGCGTGTATGAACCTACAGCCCTCTCTC 1220
1021 TTGAGCCTGTACAGGTGTGTATATGTAAGTCCATAGGTGATGATGATGATGATGAT 1080
|||||
Db 1221 TTGAGCCTGTACAGGTGTGTATATGTAAGTCCATAGGTGATGATGATGATGATGAT 1280
1081 TACACAGGGTTTACAAATTTGTAATGATTTCTACAAATTTGAACCCAGATTTGGAGAGT 1140
|||||
Db 1281 TACACAGGGTTTACAAATTTGTAATGATTTCTACAAATTTGAACCCAGATTTGGAGAGT 1340
1141 ATTCCGATGCTTATGAAGAACTTACAGGTGATGATGATGATGATGATGATGATGAT 1200
|||||
Db 1341 ATTCCGATGCTTATGAAGAACTTACAGGTGATGATGATGATGATGATGATGATGAT 1400
1201 CTAAACCCCTGGACATGTGCGCACCTGAGAACTTGAATTTAAGAGAGTCCATGTCATTGCA 1260
|||||
Db 1401 CTAAACCCCTGGACATGTGCGCACCTGAGAACTTGAATTTAAGAGAGTCCATGTCATTGCA 1460
1261 AAGAAATGATAGTGAAGGTTAAGTTCTTTGTAATTTGTAATTTGTAATTTGTAATTTG 1320
|||||
Db 1461 AAGAAATGATAGTGAAGGTTAAGTTCTTTGTAATTTGTAATTTGTAATTTGTAATTTG 1520
1321 AATTAAGTCTTTTCTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
|||||
Db 1521 AATTAAGTCTTTTCTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1580
1381 AAGTTATATTTTCAGGTATATGTTTCTGTGCAAGAGTTTGTAAATTTATTTGTGCTAT 1440
|||||
Db 1581 AAGTTATATTTTCAGGTATATGTTTCTGTGCAAGAGTTTGTAAATTTATTTGTGCTAT 1640
1441 AGTATTTGATTTCAAAATATTTAAATATGCTCACTGTTGACATATTTAAATTTAAATG 1500
|||||
Db 1641 AGTATTTGATTTCAAAATATTTAAATATGCTCACTGTTGACATATTTAAATTTAAATG 1700
1501 TACAGATGTAATTTTACTGTGACACTTTGTAATTTCCCTGAGAGTACTGATGAGAGGG 1560
|||||
Db 1701 TACAGATGTAATTTTACTGTGACACTTTGTAATTTCCCTGAGAGTACTGATGAGAGGG 1760
1561 GCAGAAATACGTGTTCTGCTGACCAACATGATGATTTCTTATTTCTTAACTTAATA 1620
|||||
Db 1761 GCAGAAATACGTGTTCTGCTGACCAACATGATGATTTCTTATTTCTTAACTTAATA 1820
1621 GAGTCTTCAG 1630
|||||
Db 1821 GAGTCTTCAG 1830

RESULT 5
AR062119
LOCUS AR062119 2295 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5843678.
ACCESSION AR062119
VERSION AR062119.1 GI:5989810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.

TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1. 2295
BASE COUNT 648 a 487 c 538 g 622 t
ORIGIN

Query Match 99.98; Score 1628.4; DB 6; Length 2295;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 CCGGGGTCACACAGAGGGGTCGGTGCACCCCGGCTTGTGACCGGCTCCGGGCGCCG 60
DB 222 CCGGGGTCACACAGAGGGGTCGGTGCACCCCGGCTTGTGACCGGCTCCGGGCGCCG 281
QY 61 CACCGCGCGCTCCCGGCTCCGTCATGTTCTGTCGCTGCGGCTGCGGCTGCGGCTGCG 120
DB 282 CACCGCGCGCTCCCGGCTCCGTCATGTTCTGTCGCTGCGGCTGCGGCTGCGGCTGCG 341
QY 121 TCTGCAGCATGCTCTGTTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 180
DB 342 TCTGCAGCATGCTCTGTTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 401
QY 181 AAGACAGCATGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 240
DB 402 AAGACAGCATGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 461
QY 241 ACTGCAGCTCTGAGAGTGAAGACACACTGACTGCTCTGAGAGAGATGAACAGCTT 300
DB 462 ACTGCAGCTCTGAGAGTGAAGACACACTGACTGCTCTGAGAGAGATGAACAGCTT 521
QY 301 TTCAGGGGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 522 TTCAGGGGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 581
QY 361 CTCGAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 582 CTCGAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
QY 421 AGCCATTTGACACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 480
DB 642 AGCCATTTGACACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 701
QY 481 CTCCTGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 540
DB 702 CTCCTGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 761
QY 541 ACGGAAACTAAGGTTTAACTAAGGTTTAACTAAGGTTTAACTAAGGTTTAACTAAGGTTT 600
DB 762 ACGGAAACTAAGGTTTAACTAAGGTTTAACTAAGGTTTAACTAAGGTTTAACTAAGGTTT 821
QY 601 GGCATTCAGAAACATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 822 GGCATTCAGAAACATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
QY 661 TTTAAACCGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGAGAGAGAGAG 720
DB 882 TTTAAACCGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGAGAGAGAGAG 941
QY 721 ACTGTCGCGCAATTCCTGATTCATCTTATTCATTAATGTTGGGGGATTTTCAACG 780
DB 942 ACTGTCGCGCAATTCCTGATTCATCTTATTCATTAATGTTGGGGGATTTTCAACG 1001
QY 781 TCCGAGCTGTTGAAGAAATTTAGCATTCAGAGTGCACACCTTCCCTGCTGATCCGAGATC 840
DB 1002 TCCGAGCTGTTGAAGAAATTTAGCATTCAGAGTGCACACCTTCCCTGCTGATCCGAGATC 1061
QY 841 AAGATCGGAGCTTGTGGGGCTTTCAAAAGTTGAGAGATAGAGTGAAGTCAATTTGCGTG 900
DB 1062 AAGATCGGAGCTTGTGGGGCTTTCAAAAGTTGAGAGATAGAGTGAAGTCAATTTGCGTG 1121
```

```
QY 901 GAACATTAGCATGATGCTGCTAGATGTTTGGAACTCTTTAAAAATGATGATGCTAT 960
DB 1122 GAACATTAGCATGATGCTGCTAGATGTTTGGAACTCTTTAAAAATGATGATGCTAT 1181
QY 961 ACATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 1182 ACATGTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1241
QY 1021 TTGAGCTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
DB 1242 TTGAGCTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1301
QY 1081 TACACAACGGTTTAACTAATTTGATGATTTCTTAAATTTGAACCGATTTGGAGAGCT 1140
DB 1302 TACACAACGGTTTAACTAATTTGATGATTTCTTAAATTTGAACCGATTTGGAGAGCT 1361
QY 1141 ATTCGATGCTTATGAAGAACTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 1362 ATTCGATGCTTATGAAGAACTTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1421
QY 1201 CTAACCCCTGGACATGTCGCTGACAGTGTGAACCTTGAATTTAAGAGATGCCATGTCATTGCA 1260
DB 1422 CTAACCCCTGGACATGTCGCTGACAGTGTGAACCTTGAATTTAAGAGATGCCATGTCATTGCA 1481
QY 1261 AAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1482 AAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1541
QY 1321 AATTAAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
DB 1542 AATTAAGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1601
QY 1381 AAGTTATATTTACAGTGTATGTTTCTGTCGAAAGTTTGTAAATTAATTAATTTGCTAT 1440
DB 1602 AAGTTATATTTACAGTGTATGTTTCTGTCGAAAGTTTGTAAATTAATTAATTTGCTAT 1661
QY 1441 AGTATTTATTTCAAAATTTTAAATTTCTCAGCTGTGACATTTTAAATTTTAAATTT 1500
DB 1662 AGTATTTATTTCAAAATTTTAAATTTCTCAGCTGTGACATTTTAAATTTTAAATTT 1721
QY 1501 TACAGATGATTTTAACTGTCGACCTTGTATTTCCCTGGAAGTACTGTAAGAGGG 1560
DB 1722 TACAGATGATTTTAACTGTCGACCTTGTATTTCCCTGGAAGTACTGTAAGAGGG 1781
QY 1561 GCAGAAATCTGTTCTGTTGACACCATGTAATTTCTTTATTTCTTTTAACTTAATA 1620
DB 1782 GCAGAAATCTGTTCTGTTGACACCATGTAATTTCTTTATTTCTTTTAACTTAATA 1841
QY 1621 GAGTCTTCAG 1630
DB 1842 GAGTCTTCAG 1851
```

RESULT 6
AF053713 2299 bp mRNA Linear ROD 09-MAY-1998
LOCUS AF053713
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053713
VERSION AF053713.1 GI:3057147
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2299)
Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Caparrelli, C., Eli, A.,
Olan, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J., and Boyle, W.-J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)

MEDLINE 98227661
REFERENCE 2 (bases 1 to 2299)
AUTHORS Boyle, M. J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA

FEATURES
Source Location/Qualifiers
1..2299

CDS
/organism="Mus musculus"
/db_xref="taxon:10090"
170..1120
/function="regulates osteoclast differentiation and
activation"
/product="osteoprotegerin ligand"
/protein_id="AAC4013.1"
/db_xref="GI:3057148"

BASE COUNT 641 a 494 c 541 g 623 t
ORIGIN
GGFELRAGEISIOVNSPLDDODATFCAKXVDID"
ICFHHETSGSVPTDYQLMYVYKTSIKIPSSHLKGGSTKMSNSEPHFYSIN
AOPFAHLJINAAISIPSGSHVTLSSMYHLDGMAKISMTLSNGLRYNODGFYLYAN
STLESDTLDPDSCKRMQAFQGAQVKELOHIVQFQSGAPAMMEGSLDVAQKQPE
ASRSMFLALGLGIVGYSIALFLYRAQDPKRISEDSTHCTRLRLHENDLGD
/translation="MRASRDYKYLRSSEEMSGSPVPHREGPLHAPAPAPPA
ASRSMFLALGLGIVGYSIALFLYRAQDPKRISEDSTHCTRLRLHENDLGD
STLESDTLDPDSCKRMQAFQGAQVKELOHIVQFQSGAPAMMEGSLDVAQKQPE
AOPFAHLJINAAISIPSGSHVTLSSMYHLDGMAKISMTLSNGLRYNODGFYLYAN
ICFHHETSGSVPTDYQLMYVYKTSIKIPSSHLKGGSTKMSNSEPHFYSIN
GGFELRAGEISIOVNSPLDDODATFCAKXVDID"

Query Match 99.9% Score 1628.4; DB 10; Length 2299;
Best Local Similarity 99.9% Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCGGGCTCCACAGAGGGTCCGCTGACACCCGCGCTTCGACACGGCTCCGGCGCCG 60
Db 234 CCGGGCTCCACAGAGGGTCCGCTGACACCCGCGCTTCGACACGGCTCCGGCGCCG 293
Oy 61 CACCGCGCGCTCCGCTGACATGTTCTCGGCCCTCTGGGCTGGGATGGGCCAGGTGG 120
Db 294 CACCGCGCGCTCCGCTGACATGTTCTCGGCCCTCTGGGCTGGGATGGGCCAGGTGG 353
Oy 121 TCTGAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 354 TCTGAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413
Oy 181 AAGACAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 414 AAGACAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473
Oy 241 ACTGAGCTCTGAGAGTGAAGACACACTGACTCTGAGAGGATGAACAAGCT 300
Db 474 ACTGAGCTCTGAGAGTGAAGACACACTGACTCTGAGAGGATGAACAAGCT 533
Oy 301 TTCAGGGGGCCGTGAGAGAACTGCAACACATTGTGGGGCCACAGGCTTCTCAGAG 360
Db 534 TTCAGGGGGCCGTGAGAGAACTGCAACACATTGTGGGGCCACAGGCTTCTCAGAG 593
Oy 361 CTCAGAGTATGAGAGGCTGATGTTGATGTGGCCCAAGGCAAGGCTGAGGCC 420
Db 594 CTCAGAGTATGAGAGGCTGATGTTGATGTGGCCCAAGGCTGAGGCC 653
Oy 421 AGCCATTGACACCTCCACATCAATGCTGACAGATCCCATGGGTTCCATAAGTCA 480
Db 654 AGCCATTGACACCTCCACATCAATGCTGACAGATCCCATGGGTTCCATAAGTCA 713
Oy 481 CTCTGCTCTTGGTACACAGATGAGGCTGGCCAAAGATCTTAACATGAGAGTAAACA 540
Db 714 CTCTGCTCTTGGTACACAGATGAGGCTGGCCAAAGATCTTAACATGAGAGTAAACA 773
Oy 541 ACGGAAACTAAGGTTTAACCAAGATGCTTATATCTGATGAGCCCAACATTTGCTTC 600
Db 774 ACGGAAACTAAGGTTTAACCAAGATGCTTATATCTGATGAGCCCAACATTTGCTTC 833
Oy 601 GGCATCATGAACATCGGAGAGCGTACTACAGTATCTTCAAGTGTATGTGCG 660

Db 834 GGCATCATGAACATCGGAGAGCGTACTACAGTATCTTCAAGTGTATGTGCG 893
Oy 661 TTAAGACAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGACAGAAA 720
Db 894 TTAAGACAGCATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGACAGAAA 953
Oy 721 ACTGCTGGGCAATTCGAATTCACATTTATTCATTAATGTGGGGATTTTCAAGC 780
Db 954 ACTGCTGGGCAATTCGAATTCACATTTATTCATTAATGTGGGGATTTTCAAGC 1013
Oy 781 TCCGAGCTGTGAAGAAATTAAGCATTCAGAGTGTCCAAACCTTCCCTGCTGATCCGATC 840
Db 1014 TCCGAGCTGTGAAGAAATTAAGCATTCAGAGTGTCCAAACCTTCCCTGCTGATCCGATC 1073
Oy 841 AAGATGCACATCTTCTGGGCTTCAAGAGTTCAAGCATAGACTGACATCTATTCGTG 900
Db 1074 AAGATGCACATCTTCTGGGCTTCAAGAGTTCAAGCATAGACTGACATCTATTCGTG 1133
Oy 901 GAACATTAAGCATGATGTCCTAGATGTTTGAAGACTTCTTAAGAAATGATGATGTCAT 960
Db 1134 GAACATTAAGCATGATGTCCTAGATGTTTGAAGACTTCTTAAGAAATGATGATGTCAT 1193
Oy 961 ACATGTGAAGCATCTAAGAGACATGGGCCACAGGTGTTGAAGACTCACAGCCCTCTC 1020
Db 1194 ACATGTGAAGCATCTAAGAGACATGGGCCACAGGTGTTGAAGACTCACAGCCCTCTC 1253
Oy 1021 TTGAGCCCTGACAGTGTGATATGTAAGTCACTAGCTGATGTTAGATTATGATGAT 1080
Db 1254 TTGAGCCCTGACAGTGTGATATGTAAGTCACTAGCTGATGTTAGATTATGATGAT 1313
Oy 1081 TACACAAAGGTTTCAATTTTGAATGATTTCTAGAAATGAACAGATTGGAGAGGT 1140
Db 1314 TACACAAAGGTTTCAATTTTGAATGATTTCTAGAAATGAACAGATTGGAGAGGT 1373
Oy 1141 ATTCGATGCTTATGAAGAAACTTACACGTGAGCTATGGAAGGGGTCAAGTCTGCTG 1200
Db 1374 ATTCGATGCTTATGAAGAAACTTACACGTGAGCTATGGAAGGGGTCAAGTCTGCTG 1433
Oy 1201 CTAACCCCTGACATGTCGACACTGAGAACCTTGAATTAAGAGATGACATGTCATTGCA 1260
Db 1434 CTAACCCCTGACATGTCGACACTGAGAACCTTGAATTAAGAGATGACATGTCATTGCA 1493
Oy 1261 AAGAAATATAGTGAAGGGTTAAGTCTTTGTAATGTTACATTCGCGTGGACCTGC 1320
Db 1494 AAGAAATATAGTGAAGGGTTAAGTCTTTGTAATGTTACATTCGCGTGGACCTGC 1553
Oy 1321 AAATAGTCTTTTCTTAATGAGAGAGAAAATATATGATTTATATATGCTTA 1380
Db 1554 AAATAGTCTTTTCTTAATGAGAGAGAAAATATATGATTTATATATGCTTA 1613
Oy 1381 AAGTTATATTCAGGTGAATGTTTCTGTGCAAAAGTTTGTAAATTAATTTTGCTAT 1440
Db 1614 AAGTTATATTCAGGTGAATGTTTCTGTGCAAAAGTTTGTAAATTAATTTTGCTAT 1673
Oy 1441 AGTATTTATTCAAATATTTTAAATATGTCACGTGTTGACATATTAATGTTTAAATG 1500
Db 1674 AGTATTTATTCAAATATTTTAAATATGTCACGTGTTGACATATTAATGTTTAAATG 1733
Oy 1501 TACAGATGATTAACATGAGTGCACATTTGTAATTCCTCGGAAGGTACGTGCTAAGGG 1560
Db 1734 TACAGATGATTAACATGAGTGCACATTTGTAATTCCTCGGAAGGTACGTGCTAAGGG 1793
Oy 1561 GCAGAAATAGTCTTCTGAGTGCACATGATGATTAATTTCTTATATCTTTAACTTAATA 1620
Db 1794 GCAGAAATAGTCTTCTGAGTGCACATGATGATTAATTTCTTATATCTTTAACTTAATA 1853
Oy 1621 GAGTCTTACG 1630
Db 1854 GAGTCTTACG 1863
RESULT 7
AR157058

LOCUS	ARI57058	2191 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	Sequence 1 from patent US 6242586.				
ACCESSION	ARI57058				
VERSION	ARI57058.1	GI:15125762.			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2191)				
TITLE	Gorman,D.M. and Mattson,J.D.				
JOURNAL	Mammalian cell surface antigens: related reagents				
FEATURES	Patent: US 6242586-A 1 05-JUN-2001;				
source	1..2191				
	/organism="unknown"				
BASE COUNT	605 a	461 c	518 g	607 t	
ORIGIN					

Query Match	99.1%;	Score 1615.8;	DB 6;	Length 2191;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1628; Conservative	0;	Mismatches	2;	Indels 1; Gaps 1.

QY	1	CGGCGCTCCACACAGAGGGTCCGTGCAACCCCGGCGCTTGTGACACGGGCTCCGGGCGCGC	60
Db	189	CGGGGTCCACACAGAGGGTCCGTGCAACCCCGGCGCTTGTGACACGGGCTCCGGGCGCGC	248
QY	61	CACCGCGCGCTCCCGGCTCCATGTTCCTGGGCGCTCTGGGGGCTGGGACTGGGCAAGTGG	120
Db	249	CACCGCGCGCTCCCGGCTCCATGTTCCTGGGCGCTCTGGGGGCTGGGACTGGGCAAGTGG	308
QY	121	TCGCGACGATCGCTCTGTTCCTGTACTTTTGAGCGCAGATGATCCTAACAGAAATTCAG	180
Db	309	TCGCGACGATCGCTCTGTTCCTGTACTTTTGAGCGCAGATGATCCTAACAGAAATTCAG	368
QY	181	AAGACAGACACACACGCTTTTATATGAATCCGAGACATCCATATGAATAACGACAGATTTTCAG	240
Db	369	AAGACAGACACACACGCTTTTATATGAATCCGAGACATCCATATGAATAACGAGTTTTCAG	428
QY	241	ACTGCATCTGGAGAGTGAAGACACACTACCTGACTCTCGACGAGGATGAACAAGCCT	300
Db	429	ACTGCATCTGGAGAGTGAAGACACACTACCTGACTCTCGACGAGGATGAACAAGCCT	488
QY	301	TTTCAGGGGGCGCTGCACAGAAGAACTGCACACATTTGGGGGCCACAGCGTTCTCAGGAG	360
Db	489	TTTCAGGGGGCGCTGCAGAGAGAACTGCACACATTTGGGGGCCACAGCGTTCTCAGGAG	548
QY	361	CTCCAGCTATGATGGAAGAGGCTCATGTGGATGTGGCCCAAGCAGAGCAACCTGAGGCC	420
Db	549	CTCCAGCTATGATGGAAGAGGCTCATGTGGATGTGGCCCAAGCAGAGCAACCTGAGGCC	608
QY	421	AGCCATTTGCACACCTCACATCAATGCTGGCAGCATCCATCGGGTTCCTCCATTAAGTCA	480
Db	609	AGCCATTTGCACACCTCACATCAATGCTGGCAGCATCCATCGGGTTCCTCCATTAAGTCA	668
QY	481	CTCTCTCTCTTTGGTACACAGATGAGGCTGGGGCAAGATCTCTAACATGACGTTAAGCA	540
Db	669	CTCTCTCTCTTTGGTACACAGATGAGGCTGGGGCAAGATCTCTAACATGACGTTAAGCA	728
QY	541	ACGGAAAACTAAGGTTTACCAAGATGGCTCTTTACCTGTACGCCAACATTTGCTTTC	600
Db	729	ACGGAAAACTAAGGTTTACCAAGATGGCTCTTTACCTGTACGCCAACATTTGCTTTC	788
QY	601	GGCATCATGAACAATCGGGAAAGCGTACTACAGACTATCTTACACTATGGTGTATGTCG	660
Db	789	GGCATCATGAACAATCGGGAAAGCGTACTACAGACTATCTTACACTATGGTGTATGTCG	848
QY	661	TTTAAAAACAGATCAAAATCCCAATTTCTCAATACGTATGAAGAGGAGCAGCAAAA	720
Db	849	TTTAAAAACAGATCAAAATCCCAATTTCTCAATACGTATGAAGAGGAGCAGCAAAA	908
QY	721	ACTGGTCGGGAATTTCTGAATTCACATTTTTCATTAATGTTGGGGATTTTTCAGC	780

Db	909	ACTGATCGGGCAATTTCTGAATTCACATTTTATTCACATAAATGTTGGGGAGATTTTTCAGC	968
Qy	781	TCCGAGCTGGTGAAGAAATTAAGATTCAGGTGTCACACCTTCCCTGCTGGATCCGATC	840
Db	969	TCCGAGCTGGTGAAGAAATTAAGATTCAGGTGTCACACCTTCCCTGCTGGATCCGATC	1028
Qy	841	AAGATGCCAGCTACTTCTGGGGCTTTCAAGTTCAGAGCATATGACATGAGACATTTGGTG	900
Db	1029	AAGATGCCAGCTACTTCTGGGGCTTTCAAGTTCAGAGCATATGACATGAGACATTTGGTG	1068
Qy	901	GAACTATTCAGATGATGATGCTAGATGTTTGGAAATCTTTAAAAAATGATGATGTCTAT	960
Db	1089	GAACTATTCAGATGATGATGCTAGATGTTTGGAAATCTTTAAAAAATGATGATGTCTAT	1148
Qy	961	ACATGTGTAAGACTCTATAAGACACATGGCCACGGTGTATGAATCAACAGCCCTCTTC	1020
Db	1149	ACATGTGTAAGACTCTATAAGACACATGGCCACGGTGTATGAATCAACAGCCCTCTTC	1208
Qy	1021	TTGAGCCGTGACAGTGTGTATATGTAAAGTCCATAGGTATGTATGATTCATGTGTAT	1080
Db	1209	TTGAGCCGTGACAGTGTGTATATGTAAAGTCCATAGGTATGTATGATTCATGTGTAT	1268
Qy	1081	TACACAAGGGTTTTCATATTTTGTATGATATTTCC - ACAAATGAACCGATTGGAGAGG	1139
Db	1269	TACACAAGGGTTTTCATATTTTGTATGATATTTCC - ACAAATGAACCGATTGGAGAGG	1328
Qy	1140	TATTCGATGCTTATGAAGAAACTTACAGTGAAGTATGGAAGGGGGTACAGTCTTG6G	1199
Db	1329	TATTCGATGCTTATGAAGAAACTTACAGTGAAGTATGGAAGGGGGTACAGTCTTG6G	1388
Qy	1200	TCTAACCCCTGGACATGTGCCACTAGAAACCTTGAAATTAAGAGATTCGATGCTATGC	1259
Db	1389	TCTAACCCCTGGACATGTGCCACTAGAAACCTTGAAATTAAGAGATTCGATGCTATGC	1448
Qy	1260	AAAGAAATCATGTGTGAAGGGGTAAAGTCTTTGAATTTGTACATTCGCGTGGACCTG	1319
Db	1449	AAAGAAATCATGTGTGAAGGGGTAAAGTCTTTGAATTTGTACATTCGCGTGGACCTG	1508
Qy	1320	CAAAATAGTCTTTTCTTAATGAGAGAGAAAAATATGATATTTTATATAAATGTCT	1379
Db	1509	CAAAATAGTCTTTTCTTAATGAGAGAGAAAAATATGATATTTTATATAAATGTCT	1568
Qy	1380	AAAGTTATATTCAGGTGTAAATGTTTCTGTGCAAAAGTTTGAATATATATTTGTGCTA	1439
Db	1569	AAAGTTATATTCAGGTGTAAATGTTTCTGTGCAAAAGTTTGAATATATATTTGTGCTA	1628
Qy	1440	TGATATTTATTCAAAATTTTAAAAATGTCCACTGTGACATATTAATGTTTAAAT	1499
Db	1629	TGATATTTATTCAAAATTTTAAAAATGTCCACTGTGACATATTAATGTTTAAAT	1688
Qy	1500	GTACAGATGTATTTAACTGTGTCACATTTGTAAATCCCTGAAGGTACTGTAGTAAGG	1559
Db	1689	GTACAGATGTATTTAACTGTGTCACATTTGTAAATCCCTGAAGGTACTGTAGTAAGG	1748
Qy	1560	GCGAGATATCTGTTTCTGCTGACACATGTAGTTATTTCTTATTTCTTTAACTTAAT	1619
Db	1749	GCGAGATATCTGTTTCTGCTGACACATGTAGTTATTTCTTATTTCTTTAACTTAAT	1808
Qy	1620	AGAGCTCTCAG 1630	
Db	1809	AGAGCTCTCAG 1819	
RESULT 8			
LOCUS	AX140162	2191 bp	DNA linear PAT 30-MAY-2001
DEFINITION	Sequence 1 from Patent EP114864.		
ACCESSION	AX140162		
VERSION	AX140162.1 GI:1427527		
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified.		
	unclassified.		

VERSION AF013170.1 GI:2411497
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2237)
AUTHORS Mong, B.R., Rho, J., Arron, J., Robinson, E., Orlicky, J., Chao, M., Kalchikov, S., Cayan, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y. and Choi, Y.
TITLE TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells
JOURNAL J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE 97460112
REFERENCE 2 (bases 1 to 2237)
AUTHORS Mong, B.R., Josien, R., Lee, S.Y., Sauter, B., Li, H.L., Steinman, R.M. and Choi, Y.
TITLE TRANCE (tumor necrosis factor [TNF]-related activation-induced cytokine), a new TNF family member predominantly expressed in T cells, is a dendritic cell-specific survival factor
J. Exp. Med. 186 (12), 2075-2080 (1997)
JOURNAL 98060869
MEDLINE 98401035
REFERENCE 3 (bases 1 to 2237)
AUTHORS Fuller, K., Wong, B., Fox, S., Choi, Y. and Chambers, T.J.
TITLE TRANCE is necessary and sufficient for osteoclast-mediated activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
JOURNAL 98401035
MEDLINE 98401035
REFERENCE 4 (bases 1 to 2237)
AUTHORS Mong, B.R., Josien, R., Lee, S.Y., Volododskaya, M., Steinman, R.M. and Choi, Y.
TITLE The TRAF family of signal transducers mediates NF-kappaB activation by the TRANCE receptor
J. Biol. Chem. 273 (43), 28355-28359 (1998)
JOURNAL 98447691
MEDLINE 98447691
REFERENCE 5 (bases 1 to 2237)
AUTHORS Mong, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y.
TITLE Direct Submission
JOURNAL Direct Submission
TITLE Direct Submission
JOURNAL Direct Submission
AUTHORS Howard Hughes Medical Institute, The Rockefeller University, 1230 York Ave., New York, NY 10021, USA
FEATURES
source 1..2237
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="14"
/map="near Rb1"
/cell_line="T cell hybridoma KMLs-8.3.5"
142..1092
/note="TNF-related ligand"
/product="TRANCE"
/codon_start=1
/protein_id="AAC71061.1"
/db_xref="GI:2411498"
/translation="MRRASRDYGYKYLSSSEMGSPVPHHGPPIHAPASAPAPPAASRSMTFLALIGLGOVVCISALFLYFAQMDPNRISDSHCFRIILRHENAGLODSTLESEDTLPDSCKMOQAFQAVQKELOHTVQRFSGAAMMGSLVDAQKQKPEAOPRHILTNASIPSGSHKVTLSMYHIDRMAMISNTLNGKILRVNDDFYLLANICFRHETSGSVPTDYLQIMYVYTSIKIPSSHLMKGGSTKMSGSEHFYSINVGFFRLRAGEELSTIOVNSPLDPQDPTFGAFVQDID"
BASE COUNT 636 a 470 c 519 g 612 t
ORIGIN

Query Match 97.4%; Score 1588.2; DB 10; Length 2237;
Best Local Similarity 99.6%; Pred. No. 0; Mismatches 3; Indels 4; Gaps 3;
Matches 1624; Conservative 0;
1 CGCGCGCCACACAGAGGTCGCTGACCCGCGCTTCTGCACCGGCTCGGCGCCG 60
|||||
206 CGCGGCTCCACACAGAGGTCGCTGACCCGCGCTTCTGCACCGGCTCGGCGCCG 265
|||||
61 CACCGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
|||||

Db 266 CACCGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
QY 121 TCTGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 326 TCTGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 385
QY 181 AAGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 386 AAGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
QY 241 ACTGACCTGAGAGTGAAGACACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 446 ACTGACCTGAGAGTGAAGACACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 505
QY 301 TTCAGGGGCGCGAGAGAGTGAAGACACATGCTGCTGCTGCTGCTGCTGCTG 360
Db 506 TTCAGGGGCGCGAGAGAGTGAAGACACATGCTGCTGCTGCTGCTGCTGCTG 565
QY 361 CTCACGCTATGATGAAGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 566 CTCACGCTATGATGAAGGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
QY 421 AGCCATTGACACGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 626 AGCCATTGACACGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685
QY 481 CTCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 686 CTCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 745
QY 541 ACGGAACCTGAAGGTTAACCAGATGGCTTCTATACCTGCTGCTGCTGCTGCT 600
Db 746 ACGGAACCTGAAGGTTAACCAGATGGCTTCTATACCTGCTGCTGCTGCTGCT 805
QY 601 GGCATCATGAACATCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 806 GGCATCATGAACATCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
QY 661 TTAACACGATCAATCAATCCCAAGTCTCATACCTGATGATGATGATGATG 720
Db 866 TTAACACGATCAATCAATCCCAAGTCTCATACCTGATGATGATGATGATG 925
QY 721 ACTGTCGGGCAATTCGAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 926 ACTGTCGGGCAATTCGAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
QY 781 TCCGAGCTGTGAAGAAATTAAGATTCAGTGTCCAAACCTTCCCTGCTGATC 840
Db 986 TCCGAGCTGTGAAGAAATTAAGATTCAGTGTCCAAACCTTCCCTGCTGATC 1045
QY 841 AAGATGCACTACTTGGGCTTCAAGATTCAGGATGATGATGATGATGATGATG 900
Db 1046 AAGATGCACTACTTGGGCTTCAAGATTCAGGATGATGATGATGATGATGATG 1105
QY 901 GAACATTGACATGATGCTGCTGATGTTTGAAGAACTTTAAAAAATGATGATG 960
Db 1106 GAACATTGACATGATGCTGCTGATGTTTGAAGAACTTTAAAAAATGATGATG 1165
QY 961 ACATGTGTAAGACTGTAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 1166 ACATGTGTAAGACTGTAAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225
QY 1021 TTGAG-CCGTGACAGTGTGTATGTAAGTCAATGATGATGATGATGATGATG 1079
Db 1226 TTGAGCCCTGTAAGAGTGTGTATGTAAGTCAATGATGATGATGATGATGATG 1285
QY 1080 TTACACAAGGTTTACATTTTGAATGATTTCTGTAAGTGAACCAAGATTTGG 1139
Db 1286 TTACACAAGGTTTACATTTTGAATGATTTCTGTAAGTGAACCAAGATTTGG 1345
QY 1140 TATTCGATGCTTATGAAGAACTTACAGTGAAGTATGGAAGGGGTCACAGTCT 1199
Db 1346 TATTCGATGCTTATGAAGAACTTACAGTGAAGTATGGAAGGGGTCACAGTCT 1404

OY	465	GGTTCACATAAGCACTCTGTCTCTTGGTACACAGATGAGGCGTGGCCAAAGATCTT	524
Db	158	GGTTCACATAAGCACTCTGTCTCTTGGTACACAGATGAGGCGTGGCCAAAGATCTT	217
OY	525	AACATGACGTTTAAGCAACGGAATACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC	584
Db	218	AACATGACGTTTAAGCAACGGAATACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC	277
OY	585	GCCAAACATTTGCTTGGGCATCATGAAACATCGGGAAGCGTACTCTACACATATCTTCAG	644
Db	278	GCCAAACATTTGCTTGGGCATCATGAAACATCGGGAAGCGTACTCTACACATATCTTCAG	337
OY	645	CTGATGCTGTAATGTCGTTTAAACACGATCAAAATCCCAAGTTCTGATTAACCTGATGANA	704
Db	338	CTGATGCTGTAATGTCGTTTAAACACGATCAAAATCCCAAGTTCTGATTAACCTGATGANA	397
OY	705	GGAGGAGACACGAAAAACCTGTGCGGCAATTTCGAATTCACATTTTATTCGCATTAATGT	764
Db	398	GGAGGAGACACGAAAAACCTGTGCGGCAATTTCGAATTCACATTTTATTCGCATTAATGT	457
OY	765	GGGGGATTTTTCGAAGCTCCGACGCTGTGAAGAAATTAGCAATTCAGGTGTCCAAACCCCTTC	824
Db	458	GGGGGATTTTTCGAAGCTCCGACGCTGTGAAGAAATTAGCAATTCAGGTGTCCAAACCCCTTC	517
OY	825	CTGCTGGATCCGGATCAAGATGGAGCATTTTGGGGCTTTCAAATTTGAGGACATAGAC	884
Db	518	CTGCTGGATCCGGATCAAGATGGAGCATTTTGGGGCTTTCAAATTTGAGGACATAGAC	577
OY	885	TGACACTCATTTGCTGGACATTTAGCATGGATGTCTCTAGATGTTTGGAAACCTTCTTAA	944
Db	578	TGACACTCATTTGCTGGACATTTAGCATGGATGTCTCTAGATGTTTGGAAACCTTCTTAA	637

Db	638	AATGATGATGTCTATACATGTAAGACACTACTAAGACAGACATGGCCACAGGTGTATGAAA	697
QY	1005	CTCACAGCCCTCTCTCTTTGAGCCCTGTACAGGTTGTGTATGTAAAGTCATAGGTGATG	1064
Db	698	CTCACACCCCTCTCTCTTTGAGCCCTGTACAGGTTGTGTATGTAAAGTCATAGGTGATG	757
QY	1065	TTATATTCATGTGATTTACACAAACGGTTTTACAAATTTTGTATGATTTTCTAGAAATTGAA	1122
Db	758	TTATATTCATGTGATTTACACAAACGGTTTTACAAATTTTGTAAAGATTTCTCGAAATTGAA	817
QY	1125	CCAGATTTGGAGAGAGGTATTTCCGATGCTTATGAAAAAATTACACGTAGCTATGGAAGGAG	1188
Db	818	CCAGATTTGGAGAGAGTATTTCCGATGCTTATGAAAAAATTACACGTAGCTATGGAAGGAG	877
QY	1185	GTCAACAGTCTCTGGGTCTAAACCCCTGGACATGTGCCACTGAGAACCTTGAAATTAAGAG	1244
Db	878	GTCAACAGTCTCTGGGTCTAAACCCCTGGACATGTGCCACTGAGAACCTTGAAATTAAGAG	937
QY	1245	ATGCGATGTCTATGCAAAAGAAATGATAGTGTGAAGGTTAAAGTCTCTTTGAAATGTGTACA	1304
Db	938	ATGCGATGTCTATGCAAAAGAAATGATAGTGTGAAGGTTAAAGTCTCTTTGAAATGTGTACA	997
QY	1305	TTGGCGTGGGACCTGCAAATAAGTTCTTTTCTTAATGAGAGAGAAAAATATATGAT	1364
Db	998	TTGGCGTGGGACCTGCAAATAAGTTCTTTTCTTAATGAGAGAGAAAAATATATGAT	1057
QY	1365	TTTTATATTAATGTCTAAAGTTATATTTACAGGTGTAAATGTTTCTGTGCAAAAGTTTGTGA	1422
Db	1058	TTTTATATTAATGTCTAAAGTTATATTTACAGGTGTAAATGTTTCTGTGCAAAAGTTTGTGA	1117
QY	1425	ATTATATTTGTGCTATAGTATTTTGATTTCAAAAATTTTAAAAAATGTCTCACTGTGACATA	1484
Db	1118	ATTATATTTGTGCTATAGTATTTTGATTTCAAAAATTTTAAAAAATGTCTCACTGTGACATA	1177

Db 1178 TTTAATGTTTAAATGTACAGATGATTAACTGGTCACCTTG-AAATTCCCTGAAGGT 1236

|||||
Db 1237 ACTGTCGTAAGGAGGAGAACTGCTTCTGTCGACACATGAGTTATTTCTTAT 1296
OY 1605 TCCTTTAACTTAATAGAGCTTCAG 1630
|||||
Db 1297 TCCTTTAACTTAATAGAGCTTCAG 1322
|||||
RESULT 11
AB022036S4 2029 bp DNA linear ROD 03-APR-2001
LOCUS Mus musculus DNA for osteoclast differentiation factor, exon 5,
DEFINITION complete cds.
ACCESSION AB022039
VERSION AB022039.1 GI:4127268
KEYWORDS osteoclast differentiation factor.
SEGMENT 4 of 4
SOURCE Mus musculus (strain:129) embryonic stem cell DNA.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
Murakami,A., Ueda,M. and Higashio,K.
TITLE Cloning and characterization of the gene encoding mouse osteoclast
JOURNAL differentiation factor
MEDLINE Gene 230 (1), 121-127 (1999)
REFERENCE 2 (bases 1 to 2029)
AUTHORS Kodaira,K.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1999) Kunihiko Kodaira, Chugai Pharmaceutical
Co., LTD.; 301 Fujii, 6-19 Nakamachi, Hamanouchi, Saltama 357-0038,
Japan (E-mail:kodaira@kai.or.jp, Tel:81-33987-0594)
FEATURES
Source Location/Qualifiers
1. 2029
/organism="Mus musculus"
/strain="129"
/db_xref="taxon:10090"
/cell_type="embryonic stem cell"
join(AB022036.1:409..630,AB022037.1:169..330,
AB022038.1:146..182,AB022038.1:274..372,159..580)
CDS
/product="osteoclast differentiation factor"
/codon_start=1
/protein_id="BAA36970.1"
/db_xref="GI:4127270"
/translation="MRRASRDYKRYLRSEEMSGPGVPHBPLHPAPAPAPPA
ASRMFLALDLGQVYVCSALFLYPAQMDPRISDSYHCEYRILRHENAGLID
STLESEDLTPDSCKRMOAFQAVOKELQHTVGPORSAMEGSLDYAOKKEPAOP
FAHLTINAAIPSGSHKVTLSWYHDKWMATISNNTLSNGLRVMDSEFYLIANIC
RHHTSGSVPTDYQLMIVYVYKTSIKIPSSHNLKGGSTKRWMSNSEHFYSINVG
FKLRAGEISISIOVSNPILDDPDATYFGAEKVDID"
159..1043
exon
/number=5
/product="osteoclast differentiation factor"
BASE COUNT 620 a 334 c 412 g 663 t
ORIGIN
Query Match 70.7%; Score 1152.4; DB 10; Length 2029;
Best Local Similarity 99.8%; Pred. No. 2.5e-262;
Matches 1164; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 465 GGTTCCCAATGAAGTCACTGTCCTTGTGTACACAGATCGAGGCGCAAGATCTCT 524
|||||
Db 158 GGTTCCCAATGAAGTCACTGTCCTTGTGTACACAGATCGAGGCGCAAGATCTCT 217
|||||
OY 525 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACTGTAC 584
|||||
Db 218 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACTGTAC 277
|||||
OY 585 GCCAATTTGCTTGGCATCATGAACATCGGGAAGGCTACCTACAGACTATCTTCAG 644
|||||

Db 278 GCCAATTTGCTTGGCATCATGAACATCGGGAAGGCTACCTACAGACTATCTTCAG 337
OY 645 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 704
|||||
Db 338 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 397
|||||
OY 705 GGAGGAGACGAAACAACTGTCGGGCAATTCGAATTCCTTTTATTCATTAATGTT 764
|||||
Db 398 GGAGGAGACGAAACAACTGTCGGGCAATTCGAATTCCTTTTATTCATTAATGTT 457
|||||
OY 765 GGGGGATTTTTCAGGCTCCGAGCTGGTGAAGAATTTAGCATTCAGGTCACACCTTCC 824
|||||
Db 458 GGGGGATTTTTCAGGCTCCGAGCTGGTGAAGAATTTAGCATTCAGGTCACACCTTCC 517
|||||
OY 825 CTGCTGATCCGGAATCAAGATGCGACGATCTTGGGGCTTCAAGTTACAGACATGAC 884
|||||
Db 518 CTGCTGATCCGGAATCAAGATGCGACGATCTTGGGGCTTCAAGTTACAGACATGAC 577
|||||
OY 885 TGAGACTATTTTCGTTGGAACATTTAGCATGATGTCCTGATGATGTTGGAACTTCTTAAA 944
|||||
Db 578 TGAGACTATTTTCGTTGGAACATTTAGCATGATGTCCTGATGATGTTGGAACTTCTTAAA 637
|||||
OY 945 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
|||||
Db 638 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697
|||||
OY 1005 CTCACAGCCCTCTCTCTGAGGCTGTACAGGTTGTATATGTAAGTTCATAGTGTATG 1064
|||||
Db 698 CTCACAGCCCTCTCTCTGAGGCTGTACAGGTTGTATATGTAAGTTCATAGTGTATG 757
|||||
OY 1065 TTAGATTTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1124
|||||
Db 758 TTAGATTTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 817
|||||
OY 1125 CCAGATTGGGAGAGGATATTCGATGCTTATGAAACCTTACACGTAGCTATGAAAGGG 1184
|||||
Db 818 CCAGATTGGGAGAGGATATTCGATGCTTATGAAACCTTACACGTAGCTATGAAAGGG 877
|||||
OY 1185 GTACAGGCTCTGAGGCTGACACCTGACAGTGTGACACCTGACACCTGAAATTAAGAG 1244
|||||
Db 878 GTACAGGCTCTGAGGCTGACACCTGACAGTGTGACACCTGACACCTGAAATTAAGAG 937
|||||
OY 1245 ATGCCATGTCATTTGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1304
|||||
Db 938 ATGCCATGTCATTTGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
|||||
OY 1305 TTGCGCTGGGACCTGCAATAATAGTCTTTTCTTAATGAGGAGAGAAATATATGAT 1364
|||||
Db 998 TTGCGCTGGGACCTGCAATAATAGTCTTTTCTTAATGAGGAGAGAGAAATATATGAT 1057
|||||
OY 1365 TTTTATATATGCTTAAGATTAATTTTCAGGCTGATGTTCTGTCGCAAGTTTGTAA 1424
|||||
Db 1058 TTTTATATATGCTTAAGATTAATTTTCAGGCTGATGTTCTGTCGCAAGTTTGTAA 1117
|||||
OY 1425 ATTATATTTGCTCTATGATTAATTTGATTCAAATATTTTAAATATGCTCAGCTGTCACATA 1484
|||||
Db 1118 ATTATATTTGCTCTATGATTAATTTGATTCAAATATTTTAAATATGCTCAGCTGTCACATA 1177
|||||
OY 1485 TTTTATGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544
|||||
Db 1178 TTTTATGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1236
|||||
OY 1545 ACTGCTAGCTAAGGCGGCAATACGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1604
|||||
Db 1237 ACTGCTAGCTAAGGCGGCAATACGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296
|||||
OY 1605 TCCTTTTAACTTAATAGAGCTTCAG 1630
|||||
Db 1297 TCCTTTTAACTTAATAGAGCTTCAG 1322
|||||
RESULT 12
AF053712

LOCUS AF053712 2271 bp mRNA linear PRI 09-MAY-1998
DEFINITION Homo sapiens osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J. and Boyle, W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submision
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES
source location/Qualifiers
1..2271
/organism="Homo sapiens"
/db_xref="taxon:9606"
185..1138
/function="regulates osteoclast differentiation and
activation"
/codon_start=1
/product="osteoprotegerin ligand"
/protein_id="AAC39731.1"
/db_xref="GI:3057146"
/translation="MRASRDYTKYLRGSEMGGRGPRAPHEGPIAHPPAPHPPPA
SRSMFVALIGLIGQVYCVSLFFFRANDPNPISDEGTCITRIILHBNADFDT
TLSDOTRLIPDSCKRIKQAFQAVQKLOHIVSQHRAKAVDSDWDLARSKL
EADPPAHLLTINATDIPSGSHVSLSSWHDGMKISMPEFNSNKLIVNODFEYLYA
NICRHHETSGDLATLEYLQMLVYVTKTSIKIPSSHTLMKGSTKXMSGNSBFHYYSIN
VGFFPKLHSGEISIEVSNPLDPDPAFYGFAPKVRDID"
BASE COUNT 658 a 462 c 522 g 629 t
ORIGIN
Query Match 57.6%; Score 939.6; DB 9; Length 2271;
Best Local Similarity 78.1%; Pred. No. 6.5e-212;
Matches 1285; Conservative 0; Mismatches 314; Indels 47; Gaps 11:
OY 1 CCGGCGTCCACACAGAGGTCCGCTGCACCCCGCCCTTCTGACCGCGCTCCGGCGCGC 60
DB 249 CCGGAGCCCGGACAGAGGCGCCCTGACGCGCCCGC---CCCGCGCTCGCGCGCACGAC 305
OY 61 CACCGCGCGCTCCGCTGCATGTTCTGAGGCGCTCTGGGCGTGGAGTGGCGCCAGTGG 120
DB 306 CCGCGCGCGCTCCGCTGCATGTTCTGAGGCGCTCTGGGCGTGGAGTGGCGCGAGTGG 365
OY 121 TCTGAGAGTGGCTCTGTTCTCTGTAATTCGAGCGCAGATGGATCTTAACAGAAATATCAG 180
DB 366 TCTGAGAGTGGCTCTGTTCTCTGTAATTCGAGCGCAGATGGATCTTAATAGAAATATCAG 425
OY 181 AAGACAGAGTCACTGCTTTTATAGAAATCTGAGAGTCTCATGAAACCCAGATTTGCAGG 240
DB 426 AAGATGGAGTCACTGCAATTAATAGAAATTTTGAAGCTCATGAAATGCAAGATTTTTCAGG 485
OY 241 ACTGCACTCTGAGAGTGAAGACAC-----ACTACCTGAGTCTCCGCGAGGAGATGAAC 294
DB 486 ACACAACTCTGAGAGTGAAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 545
OY 295 AAGCTTTTCAGAGGCGCTGCGAGAAAGTGAACATTTGGGGCGCACAGCGCTTCT 354
DB 546 AAGCTTTTCAGAGGCGCTGCGAGAAAGTGAACATTAATTAATTAATTAATTAATTAATTA 605

OY 355 CAGAGCTCCACGATGATGAAGAGGCTCATGTTGATGTGGCCCGACGAGGACAGCTG 414
DB 606 GAGCAGAGAAAGCATGGTGGATGGCTCATGGTTAGATCTGGCCAGAGAGAGCATGGT 665
OY 415 AGGCCAGCATTTTGCACACCTCACCATCATATGCTGCCAGCATCCCATCGGGTTCCATA 474
DB 666 AAGCTCAGCGCTTTGCTCATCTCACTATTAATGCCAGCATCCCATCTGTTCCATA 725
OY 475 AAGTCACTCTGCTCTTGTGTACCGAGTCCAGAGTGGCGCCAGAGTCTTAACATGACGT 534
DB 726 AAGTCACTCTGCTCTTGTGTACCGAGTCCAGAGTGGCGCCAGAGTCTTAACATGACGT 785
OY 535 TAAGACAGGAAATTAAGGGTTAACAAGATGGCTCTTAATTAATTAATTAATTAATTAAT 594
DB 786 TTAGCAATGGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 845
OY 595 GCTTTGCGCATCATGAACATCGGAGACGTAACCTACAGATCTTACAGTATGCTGT 654
DB 846 GCTTTCAGATCATGAACATCGGAGACGTAACCTACAGATCTTACAGTATGCTGT 905
OY 655 ATGCTGTTAAACCGCATCAAAATCCCAAGTTCATTAACCTGATGAAGAGGACCA 714
DB 906 AGCTCAGTAAACCGCATCAAAATCCCAAGTTCATTAACCTGATGAAGAGGACCA 965
OY 715 CGAAATGCTGCGGCAATTCGTAATTCGATTAATTAATTAATTAATTAATTAATTAAT 774
DB 966 CCAATATTTGGTCAGAGGAATTCGTAATTCGATTAATTAATTAATTAATTAATTAATTA 1025
OY 775 TCAGCTCCGAGCTGGTGAAGAAATTAACATTAAGGTGCCAACCTTCCCTGCTGATC 834
DB 1026 TTAAGTACGCTGCGAGAGAAATTAACATTAAGGTGCCAACCTTCCCTGCTGATC 1085
OY 835 CGGATCAGATGCGGAGTCTTGGGCTTCAAGATTCAGAGCATTAAGTACATGACATCAT 894
DB 1086 CGGATCAGATGCGGAGTCTTGGGCTTCAAGATTCAGAGCATTAAGTACATGACATCAT 1145
OY 895 TTCTGGAACATTAAGCATGATGTCCTAGATGTTTGAACCTTCTTAATAA-----AT 947
DB 1146 TTTTGGAGGTT---ATGATTTCTGAGATGTTTGAACCTTCTTAATAA-----AT 1202
OY 948 GGATGATGTCATACATGATGTAAGACATTAAGACATTAAGACATTAAGACATTAAGAC 1007
DB 1203 GAAAGATGTAATAGGTGTGAGACATTAAGACATTAAGACATTAAGACATTAAGACAT 1262
OY 1008 ACAGCCCTCTCTTGAAGCCGTACAGGTTGTGTAATGTAATGTAATGTAATGTAATGTA 1067
DB 1263 AGTATCCATGCTCTTGAAGCCGTACAGGTTGTGTAATGTAATGTAATGTAATGTAAT 1322
OY 1068 GATTCAATGTTG-ATTACCAAGGTTTACAAATTTTGAATGTAATGTAATGTAATGTAATG 1126
DB 1323 GACTCATGTTGTGTACCAATGTTTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 1382
OY 1127 AGATTGGAGAGGTAATTCGATGCTTAAGAAACCTTAACAGTGAAGTATGAAGAGGGGT 1186
DB 1383 AGATTGGAGAGGTAATTCGATGCTTAAGAAACCTTAACAGTGAAGTATGAAGAGGGGT 1440
OY 1187 CACAGTCTGCTGCTTAACCCCTGAGACATGCGCACAGAGAACCTTAATTAAGAGAT 1246
DB 1441 -----TTGCTCCCTGCTGATGCTGCTTCCGAGT-TGAAGTGGAGAGGGT 1485
OY 1247 GCGATGTCATGCAAGAAATGATAGTGAAGGTTAAGTCTTCTTGAATGTAATGTAATG 1306
DB 1486 GTCACT-AGGCAATTTGAAGGATCATCTGAAGGGCAAAATTTCTTGAATGTAATGTAAT 1364
OY 1307 GCGCTGGAGCTGCAAAATTAAGTCTTTTCTTAATGAGAGAGAAATATATGTAATTT 1366
DB 1366 ATGCTGAACCTGCAAAATTAAGTCTTTTCTTAATGAGAGAGAAATATATGTAATTT 1600
OY 1367 TTAATATGCTTAAGTATTAATTTAGGTATGTTTCTGAGCAAAATTTTGTAAAT 1426
DB 1601 TTAATATATCTTAAGTATTAATTTAGGTATGTTTCTGAGCAAAATTTTGTAAAT 1660
OY 1427 TATATTTGCTATAGTATTTGATCAAAATATTTAAATATGTCACGTTGACATATTT 1486

|||||
Db 1661 TATATTTGTCTAGTATTGATTCAAAATTTAAATTAAGTCTGCTGTGACATATT 1720
QY 1487 TAAATGTTTAAATGATACAGATGATTTAACTGTGACATTTGTAATTCCTG----AA 1541
|||||
Db 1721 TAAATGTTTAAATGATACAGATTTAACTGTGACATTTGTAATTCCTGCGGAAAA 1780
QY 1542 GGTACTGTAGCTAAGAGGGGAGAAATGCTTTTGTGCTGACCATGATGTTATTTCTT 1601
Db 1781 CTTCGACCTAAGAGGGGAGAAATGCTTTTCTTAAATCAATGACATATTTCTT 1840
QY 1602 TATCTTTTAACTTAAATGACCTT 1627
Db 1841 CGTCTTTTAAATGATTAATGATTTT 1866
RESULT 13
AF019047 2201 bp mRNA linear PRI 22-NOV-1997
LOCUS Homo sapiens receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2201)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D., and
Galibert,L.
A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
Nature 390 (6566), 175-179 (1997)
98032977
2 (bases 1 to 2201)
Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., Dubose,R. and Galibert,L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
FEATURES
source Location/Qualifiers
1..2201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="13q14"
1..2201
/gene="RANKL"
129..1082
/gene="RANKL"
/note="receptor activator of nuclear factor kappa B
ligand"
/codon_start=1
/product="RANKL"
/protein_id="AAB86811.1"
/db_xref="GI:2612922"
/translation="MRRASRDYTKLRSGSEMGSGPRAPHEPLIAPPAPHPAPPA
SRSMFVALIGLIGVVCVALFFYFRQMDPNRISSEDTGCTITLRLHENADPDT
TLESODTKLIPSCRRIKAFQGAQVOKELQHLIVGQHLRAEKAMDGSLDLAKRSKL
EAOPFAHLTINATDIPSGSHKYSLSMYHDRGMARISNMTFENGKLIYNODGFYLYA
NICPHEHETSGDLATEYLOIMYVTKTSIKIPSSHTLMKSGSTKYWGSNSEHFYSIN
VGFFKLNSGEIEISIEVSNPSILDDPDQATYTGAKRVNRID"
BASE COUNT 658 a 429 c 497 g 617 t
ORIGIN
Query Match 57.0%; Score 928.6; DB 9; Length 2201;
Best Local Similarity 78.0%; Pred. No. 2,6e-209;
Matches 1285; Conservative 0; Mismatches 314; Indels 48; Gaps 12;
QY 1 CCGGCGTCCACACAGAGGCTCGCTGCACCCCGCGCTTGTGACCGGCTCGGCGCGC 60

|||||
Db 193 CCGAGAGCCCGCAGAGAGGCCCCCTGCACGCCCCG----CGCGCGCTCGGCGCGCACAC 249
QY 61 CACCCGCGCGCTCCCGCTGCATGTTCCCTGGGCGCTGGAGACTGGCGAGCTGG 120
Db 250 CCCCCGCGCGCTCCCGCTGCATGTTCCCTGGGCGCTGGAGACTGGCGAGCTGG 309
QY 121 TCTGACGATCGCTCTGTTCTGCTGACTTTTCGAGCGCAGATGATCTTACAGAAATACG 180
Db 310 TCTGACGATCGCTCTGTTCTGCTGACTTTTCGAGCGCAGATGATCTTACAGAAATACG 369
QY 181 AAGACGACTGCTGCTTTTATGAAATCTGAGACTCCATGAAACGCGATTTTGCAG 240
Db 370 AAGATGCGACTGCTGCTTTTATGAAATCTGAGACTCCATGAAACGCGATTTTGCAG 429
QY 241 ACTGCACTGAGAGTGAAGACAC-----ACTAGCTGACTCGCAGAGAGTGAAC 294
Db 430 ACACACTCTGAGAGTGAAGACAC-----ACTAGCTGACTCGCAGAGAGTGAAC 489
QY 295 AAGCTTTCAAGGGGCGCGTGCAGAAAGACTGCAACACATTTGCGGCCACAGCGCTTCT 354
Db 490 AGGCTTTCAAGGAGCTGTGCAGAAAGAAATACACATATCTGTGATCACAGCACATCA 549
QY 355 CAGAGCTCAGCTATGATGAGAGGCTCATGTTGATGATGATGATGATGATGATGATGATG 414
Db 550 GAGCAGAGAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609
QY 415 AGGCGCAGCTTTTGCACACTGACACATCAATGCTGACAGATCCATCGGTTCCATA 474
Db 610 AAGCTCAAGCTTTTGTCTATCTCATCTATTAATGACCGAGATCCATCGGTTCCATA 669
QY 475 AAGTCACTCTGCTCTTGTGATACAGATGAGAGCTGAGGCTGGCCAAATCTTAACTGACGT 534
Db 670 AAGTCACTCTGCTCTTGTGATACAGATGAGAGCTGAGGCTGGCCAAATCTTAACTGACGT 729
QY 535 TAAGCAAGGAAACTAGAGGTTAAACCAAGATGCTTATTAAGTCAAGCAAGATTT 594
Db 730 TAAGCAAGGAAACTAGAGGTTAAACCAAGATGCTTATTAAGTCAAGCAAGATTT 789
QY 595 GCTTTCGCGATCAGTGAACATCGGAGAGGCTGACAGATCTTCAAGTATCTTCAAGTATG 654
Db 790 GCTTTCGCGATCAGTGAACATCGGAGAGGCTGACAGATCTTCAAGTATCTTCAAGTATG 849
QY 655 ATGCTGTTAAACACGATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGAGGAGCA 714
Db 850 ACGTCACTAAACACGATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGAGGAGCA 909
QY 715 CGAAATACCTGCTCGGCAATCTGAATTCGACTTTTATTCATTAATTTGGGGGATTTT 774
Db 910 CGAAATACCTGCTCGGCAATCTGAATTCGACTTTTATTCATTAATTTGGGGGATTTT 969
QY 775 TCAAGCTCGAGCTGCTGTAAGAAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC 834
Db 970 TTAAGTTAGCTGCTGTAAGAAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC 1029
QY 835 CGGATCAAGATCGAGCTGCTGTAAGAAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC 894
Db 1030 CGGATCAAGATCGAGCTGCTGTAAGAAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC 1089
QY 895 TTTCGGAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC-----AT 947
Db 1090 TTTCGGAATTTAGCATTCAGGTGTCACACCTTCCTGCTGATC-----AT 1146
QY 948 GGTATGCTCTATACATCTGTGTAAGACTTAAAGACATGCGCCACAGGCTGTATGAACCTC 1007
Db 1147 GAAAGATGATATAGTGTGTGACTACTAAGAGGCAATGCGCCACAGGCTGTATGAACCTC 1206
QY 1008 ACAGCCCTCTCTTGAAGCTGTAGAGCTGTGATGATGATGATGATGATGATGATGATGATG 1066
Db 1207 AGTATCCATCTCTTGAAGCTGTAGAGCTGTGATGATGATGATGATGATGATGATGATGATG 1266
QY 1067 AGTATCCATCTCTTGAAGCTGTAGAGCTGTGATGATGATGATGATGATGATGATGATGATG 1125

Db 1267 AGACTATGCTGTTCACCAATGTTTTTAATTTGTAATGMAATTCCTAGATTAAAC 1326

Qy 1126 CAGATTGGAGAGATATTCGATGCTTATGAAAACTTACAGCTATGGAAGGGG 1185

Db 1327 CAGATTGGAGCAATTCAGGTTGACCTTATGAAAACTGATGTGGCTATGGAGGG- 1385

Qy 1186 TCACACTCTCTGGGCTTAACCCCTGGACATGCGACAGAACCTTGAATTAAGAGA 1245

Db 1386 -----TTGGTCCCTGGTCATGTGCCCCCTCGCAGC-TGAAGTGGAGAGGG 1429

Qy 1246 TGGCATGCTATTGCAAAAGAAATGATAGTGAAGGTTAAAGTTCTTTGAATTTACAT 1305

Db 1430 TGTGATCT-AGGCAATTAAGAGATCATCTGAAGGGCAAAATCTTTGAATTTACAT 1488

Qy 1306 TGGCGTGGAGACCTGCAAAATAGTTCTTTTCTAATGAGAGAAAAATATATGATAT 1365

Db 1489 CATGCTGGAACTCGCAAAAAATAC---TTTTCTAATGAGAGAG-AAAATATATGATAT 1544

Qy 1366 TTTATATATGCTTAAGATTATTTTACAGCTGAATGTTTCTGTCAGAAAGTTGTAA 1425

Db 1545 TTTATATATATCTAAAGTTATATTTCAAGATGTAATGTTTCTGCAAAAGTATGTAA 1604

Qy 1426 TTTATATTTGCTATATGATTTGATTCAAATATTTTAAATGCTCACTGTGACATAT 1485

Db 1605 TTTATATTTGCTATATGATTTGATTCAAATATTTTAAATGCTGCTGTGACATAT 1664

Qy 1486 TTTAATGTTTAAATGATGATGATTTTAACTGTGCTGCTTTGATTTCCCTG-----A 1540

Db 1665 TTTAATGTTTAAATGATGATGATTTTAACTGTGCTGCTTTGATTTCCCTGAGGAAA 1724

Qy 1541 AGTCTGCTACTAAGGGGCGAATACTGTTTCTGCTGACCATGATGTTTATTTCT 1600

Db 1725 ACTTCAGCTAAGAGAGGAAAAAATGTTGTTCTTAATATCAATGACGATATTTCT 1784

Qy 1601 TTTATCTTTTAACTTAATAGAGCTT 1627

Db 1785 TCGTCTTTTAACTTAATAGATTTT 1811

RESULT 14

E34350 951 bp DNA linear PAT 31-JAN-2002

LOCUS E34350 DNA and process for producing protein by using the same.

DEFINITION E34350

ACCESSION E34350.1 GI:18624335

VERSION E34350.1

KEYWORDS JP 2000102390-A/5.

SOURCE Mus sp.

ORGANISM Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 951)

AUTHORS Mizuno,A., Kodaira,K. and Kodaira,Y.

TITLE DNA and process for producing protein by using the same

JOURNAL Patent: JP 2000102390-A 5 11-APR-2000;

SNOW BRAND MILK PROD CO LTD,YS NEW TECHNOLOGY LAB

COMMENT OS Mus sp. (mouse)

PN JP 2000102390-A/5

PD 11-APR-2000

PR 30-SEP-1998 JP 1998292971

PI ATSUOKO MIZUNO, KUNIHICO KODAIRA, YASUOKO KODAIRA PC

C12N15/09,A61K31/00,C07K14/47,C12P21/02,C12Q1/68//C12N15/09, PC

C12R1.91),

PC (C12P21/02,C12R1.91),C12N15/00,(C12N15/00,C12R1.91) CC

PH key Location/Qualifiers

FT source 1..951

FT Location/Qualifiers

FEATURES

source 1..951

Location/Qualifiers

1..951

/organism="Mus sp."

/db_xref="taxon:10095"

BASE COUNT 231 a 267 c 248 g 205 t

ORIGIN

Query Match 54.3%; Score 885.4; DB 6; Length 951;

Best Local Similarity 99.9%; Pred. No. 3.7e-199;

Matches 886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGTCCCAACAGAGGGTCCGTCGACCCCGGCGCTTTCGACCGGCTCCGGCGCCG 60

Db 65 CCGGGTCCCAACAGAGGGTCCGTCGACCCCGGCGCTTTCGACCGGCTCCGGCGCCG 124

Qy 61 CACCCGCGCCCTCCCGCTCATGTTCTTGCCCTCTGCGGCTGGAGCTGGGCCAGTGG 120

Db 125 CACCCGCGCCCTCCCGCTCATGTTCTTGCCCTCTGCGGCTGGAGCTGGGCCAGTGG 184

Qy 121 TCTGAGCATGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 180

Db 185 TCTGAGCATGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 244

Qy 181 AAGACGACCTACCTGCTTTTATAGAAATCTGAGACTGAGACTGAGAAAGGCAATTTG 240

Db 245 AAGACGACCTACCTGCTTTTATAGAAATCTGAGACTGAGACTGAGAAAGGCAATTTG 304

Qy 241 ACTGCACTCTGAGAGTGAAGACACACTGACTGACTCTGAGAGAGATGAAGAAAGCT 300

Db 305 ACTGCACTCTGAGAGTGAAGACACACTGACTGACTCTGAGAGAGATGAAGAAAGCT 364

Qy 301 TTTACAGGGGCGGTCAGAAAGCACTGAAACATTTGTTGGGCGCACAGGCTTTCAGAG 360

Db 365 TTTACAGGGGCGGTCAGAAAGCACTGAAACATTTGTTGGGCGCACAGGCTTTCAGAG 424

Qy 361 CTCGAGCTATGAGAAAGCTCATGTTGATGTGGGCCAGGAGGCAAGGCTGAGGCGC 420

Db 425 CTCGAGCTATGAGAAAGCTCATGTTGATGTGGGCCAGGAGGCAAGGCTGAGGCGC 484

Qy 421 AGCCATTGTCACACTCCTCACTCAATGCTGCACAGATCCATCGGGTCCATTAAGTCA 480

Db 485 AGCCATTGTCACACTCCTCACTCAATGCTGCACAGATCCATCGGGTCCATTAAGTCA 544

Qy 481 CTCGTCTCTTTGGTACACGATGAGGCTGGGCGAAGATCTGTAACATGACGTTAAGCA 540

Db 545 CTCGTCTCTTTGGTACACGATGAGGCTGGGCGAAGATCTGTAACATGACGTTAAGCA 604

Qy 541 ACGGAAAACCTAAGGCTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCT 600

Db 605 ACGGAAAACCTAAGGCTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCT 664

Qy 601 GGCATCATGAACAATCGGGAAGCTACCTACAGACTATTTTCAGCTGATGGTATGTCG 660

Db 665 GGCATCATGAACAATCGGGAAGCTACCTACAGACTATTTTCAGCTGATGGTATGTCG 724

Qy 661 TTTAAACACGATCAAAATCCCAAGTTCTCATACGATGAGAAAGGAGGAGCAAGAAA 720

Db 725 TTTAAACACGATCAAAATCCCAAGTTCTCATACGATGAGAAAGGAGGAGCAAGAAA 784

Qy 721 ACTGGTGGGCAATTCGAATTCACCTTTAATTCATTAATGTTGGGGATTTTTCAGC 780

Db 785 ACTGGTGGGCAATTCGAATTCACCTTTAATTCATTAATGTTGGGGATTTTTCAGC 844

Qy 781 TCCGAGCTGGTGAAGAAATTAAGATTCAGGTGTCAACCCCTCTCTGATCCGATC 840

Db 845 TCCGAGCTGGTGAAGAAATTAAGATTCAGGTGTCAACCCCTCTCTGATCCGATC 904

Qy 841 AAGATCGGAGTACTTGGGCTTTCAGAAAGTTCAGGACATAGACTGA 887

Db 905 AAGATCGGAGTACTTGGGCTTTCAGAAAGTTCAGGACATAGACTGA 951

RESULT 15

E36388 951 bp DNA linear PAT 07-FEB-2001

LOCUS E36388 Novel protein, DNA and utilization thereof.

DEFINITION E36388

ACCESSION E36388.1 GI:13017477

VERSION

KEYWORDS	JP 1999332581-A/1.
SOURCE	Mus sp. .
ORGANISM	Mus sp.
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 951)
TITLE	Kyoji,Y.N.S.S. and Tsuda,T.M.K.R.
JOURNAL	Novel protein, DNA and utilization thereof Patent: JP 1999332581-A 1 07-DEC-1999;
COMMENT	SNOW BRAND MILK PROD CO LTD,SANKYO CO LTD OS Mus sp. (mouse) PN JP 1999332581-A/1 PD 07-DEC-1999 PF 20-OCT-1998 JP 1998316973
FEATURES	PI KYOI YAMAGUCHI,NOBUYUKI SHIMA,EIJI TSUDA,TOMONORI MORINAGA, PI KANI HIRASHIO PC C12N5/09,A61K31/00,A61K38/00,A61K45/00,C07K14/47,C07K16/18, PC C12N5/10, PC C12P21/02,G01N33/15,G01N33/566/((C12P21/02,C12R1:91), C12N15/00,PC A61K37/02, PC C12N5/00 CC FH FT FT
source	Location/Qualifiers 1..951 /organism="Mus sp." /db_xref="taxon:10095"
BASE COUNT	231 a 267 c 248 g 205 t
ORIGIN	
Query Match	54.3%; Score 885.4; DB 6; Length 951;
Best Local Similarity	99.9%; Pred. No. 3.7e-199;
Matches	886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1	CCGGCGTCCACACGAGGGTCGGTCGACACCCGGCGCTTCTGACCCGGCTCCGGGGCGCG
65	CCGGCTCCACACGAGGGTCGGTCGACACCCGGCGCTTCTGACCCGGCTCCGGGGCGCG
61	CACCGCGCGCTCCGGCTCGATGTTCTCTGAGCCCTCTCTGGGGCTGGAGCTGGGCGAAGTGG
125	CACCGCGCGCTCCGGCTCGATGTTCTCTGAGCCCTCTCTGGGGCTGGAGCTGGGCGAAGTGG
121	TCGACAGCATCGCTGTTCTGCTGACTTTGAGCGCAGATGGATCTCTAACAGATATCGAG
185	TCGACAGCATCGCTGTTCTGCTGACTTTGAGCGCAGATGGATCTCTAACAGATATCGAG
181	AAGACAGCATCGCTGTTCTGCTGACTTTGAGCGCAGATGGATCTCTAACAGATATCGAG
245	AAGACAGCATCGCTGTTCTGCTGACTTTGAGCGCAGATGGATCTCTAACAGATATCGAG
241	ACTGCACTCTGGAGAGTGAAGACACACTACTACTCTCTGACAGAGGATGAAGCAAGCCT
305	ACTGCACTCTGGAGAGTGAAGACACACTACTACTCTCTGACAGAGGATGAAGCAAGCCT
301	TTGACGGGGCGCTGTCAGAAAGAACTGCAACAACTTGGGGGGCCAGAGCGCTTCTCAGGAG
365	TTGACGGGGCGCTGTCAGAAAGAACTGCAACAACTTGGGGGGCCAGAGCGCTTCTCAGGAG
361	CTTCAGCTATGATGAAGGCTCATGTTGGATGTGAGCCAGCGAGGCAAGCCTGAGGCC
425	CTTCAGCTATGATGAAGGCTCATGTTGGATGTGAGCCAGCGAGGCAAGCCTGAGGCC
421	AGCCATTGGACACCTCAGCATCAATCTGCGCAGCATTCATCGGGTTCCCATTAAGTCA
485	AGCCATTGGACACCTCAGCATCAATCTGCGCAGCATTCATCGGGTTCCCATTAAGTCA
481	CTCTGCTCTTGGTATACAGATGAGAGGCGGCGCAAGATCTCTAACATGACGTTAAGCA
545	CTCTGCTCTTGGTATACAGATGAGAGGCGGCGCAAGATCTCTAACATGACGTTAAGCA

OY	541	ACGGAACCTAAGGTTTACCACAAATGGCTTATTACCTGTCAGGTCAGCAATTTGCTTTC	600
Db	605	ACGGAAAACTAAGGGTTTACCACAAATGGCTTATTATTACCTGTACGCCACAAATTTGCTTTC	664
OY	601	GGCATCATGAACATTCGGAGAGCTTACCTACAGACTCTATTCTTCAGCTGATGGTATGTGCG	660
Db	665	GGCATCATGAACATTCGGAGAGCTTACCTACAGACTCTATTCTTCAGCTGATGGTATGTGCG	724
OY	661	TTAAAACCGAGCATCAAAATCCCAAGTCTCATACCTGATGAAAGGAGGAGCAGCAAAA	720
Db	725	TTAAAACCGAGCATCAAAATCCCAAGTCTCATACCTGATGAAAGGAGGAGCAGCAAAA	784
OY	721	ACTGTCGGGGCAATTTCTAATTTCCACTTTTATTCACATAAATGGTGGGGGAAATTTTTCAGC	780
Db	785	ACTGTCGGGGCAATTTCTAATTTCCACTTTTATTCACATAAATGGTGGGGGAAATTTTTCAGC	844
OY	781	TCCGAGCGTGCACAAATTTAGCATTCAGGTCCCAACCCCTCCCTCTGTAGTCCGGATC	840
Db	845	TCCGAGCGTGCACAAATTTAGCATTCAGGTCCCAACCCCTCCCTCTGTAGTCCGGATC	904
OY	841	AAGATGCGACGACTTTGGGGCTTTCAAAGTTTCAGAGCATAGACTGA	887
Db	905	AAGATGCGACGACTTTGGGGCTTTCAAAGTTTCAGAGCATAGACTGA	951

Search completed: July 8, 2002, 23:50:08
Job time: 13447 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:02:26 ; Search time 408.13 Seconds

(without alignments)
6857.057 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630

Sequence: 1 CCGGCGTCCACACAGAGGT.....TAACCTAATAGATCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_032802.*
2: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
4: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
5: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
6: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
7: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
8: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
9: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
10: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
11: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
12: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
13: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
14: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
15: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
16: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
17: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
18: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
19: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
20: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
21: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
22: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
23: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1630	100.0	1630	19	AAV41377
2	1630	100.0	1630	19	AAV41371
3	1630	100.0	1630	22	AAV41371
4	1630	100.0	1630	22	AAV41371
5	1630	100.0	1630	22	AAV41371
6	1628.4	99.9	2295	19	AAV70284
7	1628.4	99.9	2295	21	AAV70284
8	1615.8	99.1	2191	19	AAV41489
9	1588.2	97.4	2237	20	AAV80224

10	1348.4	82.7	1538	19	AAV69886	Nucleic acid encod
11	1152.4	70.7	2029	21	AA39155	Mouse OBM nucleoti
12	939.6	57.6	2271	21	AA29964	DNA encoding a hum
13	939.6	57.6	2274	19	AAV70285	Human osteoprotege
14	885.4	54.3	951	19	AAV69900	Nucleotide sequenc
15	885.4	54.3	951	21	AA39156	Mouse OBM nucleoti
16	885.4	54.3	951	21	AA29965	DNA encoding a mur
17	885.4	54.3	951	21	AA29965	Osteoclast formati
18	832.8	51.1	1833	20	AAV80223	Human TRANCE encod
19	773.4	47.4	1574	22	AAV86481	Rat osteoclast dif
20	764.6	46.9	1574	22	AAH25526	Nucleotide sequenc
21	733.4	45.0	735	19	AAV69898	Nucleic acid encod
22	615	37.7	954	19	AAV41378	NF-kB receptor act
23	615	37.7	954	19	AAV41372	NF-kB receptor act
24	615	37.7	954	22	AAV41372	Human receptor act
25	615	37.7	954	22	AAV41372	Human receptor act
26	615	37.7	954	22	AAV41372	Human receptor act
27	611.8	37.5	954	22	AAV41372	Human receptor act
28	520.6	31.9	741	19	AAV69887	Human full-length
29	466	28.6	522	22	AAV69889	Nucleic acid encod
30	313.2	19.2	564	21	AAV13369	Mouse cDNA encodin
31	312.2	19.2	519	21	AA29966	DNA encoding a syn
32	312.2	19.2	519	21	AA29966	DNA encoding a syn
33	278.6	17.1	519	21	AA29969	DNA encoding a mur
34	262.4	16.1	546	21	AA29972	DNA encoding osteo
35	259.4	15.9	519	21	AA29973	DNA encoding osteo
36	247.6	15.2	564	21	AA29970	DNA encoding osteo
37	165.8	10.2	468	21	AA39153	DNA encoding osteo
38	157.8	9.7	2026	21	AA39152	Mouse OBM nucleoti
39	120.6	7.4	254	20	AAV56001	Human tumour necro
40	105.8	6.5	575	21	AAA39154	Mouse OBM nucleoti
41	58.4	3.6	656	21	AAA38005	Cell factor deriva
42	58.4	3.6	759	22	AAV18398	GH-derived leader
43	58.4	3.6	768	22	AAV18399	CMV-derived leader
44	58.4	3.6	801	22	AAV03112	Ompa signal peptid
45	58.4	3.6	846	19	AAV42205	TNF-related apopto

ALIGNMENTS

RESULT 1		
ID	AAV41377	standard; cDNA; 1630 BP.
AC	AAV41377;	
XX		
DT	08-OCT-1998	(first entry)
XX		
DE	NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.	
XX		
KW	RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;	
KW	immune response; inflammatory response; toxic shock; sepsis;	
KW	RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.	
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	3..887
FT		/*tag= a
FT		/product= "murine RANKL (ligand for RANK)"
XX		
PN	W09828426-A2.	
XX		
PD	02-JUL-1998.	
XX		
PF	22-DEC-1997;	97WO-US23775.
XX		
PR	14-OCT-1997;	97US-0064671.
PR	23-DEC-1996;	96US-0059978.
PR	07-MAR-1997;	97US-0813509.
XX		
PA	(IMMV) IMMUNEX CORP.	

Db 1561 gcagatactcttcgtgacacacatgtagttattcttcttacttcttaacttaata 1620
QY 1621 GAGTCTTCAG 1630
 |||||
Db 1621 gactcttcag 1630

RESULT 2
AAVA1371
ID AAVA1371 standard; cDNA; 1630 BP.
XX
AC AAVA1371;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW Immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 3..887
FT CDS /*tag= a
FT /product= "murine RANKL (ligand for RANK)"
XX
PN M00828424-A2.
XX
PD 02-JUL-1998.
XX
PE 22-DEC-1997; 97WO-0523866.
XX
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
PA (IMMEX) IMMEX CORP.
XX
PI Anderson DM, Gallbert LJ, Maraskovsky E;
XX
DR WPI: 1998-377655/32.
DR P-PSDB; AAM68292.
XX
PT New isolated receptor activator of necrosis factor-kappa B - useful
PT for, e.g. developing products for regulating an immune or
PT inflammatory response, treating toxic shock or sepsis
XX
PS Example 7; Pages 55-57; 80pp; English.

XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
XX activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
XX member of the tumour necrosis factor (TNF) family. Host cells transformed
XX or transfected with an expression vector comprising the RANK encoding
XX nucleic acid can be used to produce recombinant RANK protein. The soluble
XX RANK may be used for inhibiting activation of NF-kB, by contacting a cell
XX expressing membrane-associated RANK with a soluble RANK which binds to
XX RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
XX used for regulating an immune or inflammatory response. Inhibition of
XX NF-kB by RANK antagonists may be useful in ameliorating negative effects
XX of an inflammatory response that result from triggering of RANK, e.g. in
XX treating toxic shock or sepsis, graft-versus-host reactions, or acute
XX inflammatory reactions. They can also be used in adjunct therapy for
XX disease characterised by neoplastic cells that express RANK. The products
XX can also be used for detection and drug screening.

SO Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 100.0%; Score 1630; DB 19; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGCGTCCACACAGAGGATCCGCTGACCCCGGCGCTTCTGACCGGCTCCGGCGGC 60
 |||||
Db 1 ccggcggtcccaacagaggtgcgtgcaccccgcccttcgcacggctccgcgcgc 60
 |||||
QY 61 CACCCGCCGCTCCCGCTCCATGTTCTCGGCGCTCGGGGCTGGGACTGGCCAGGTGG 120
 |||||
Db 61 caccgcgcgcctcccgctccacatgcttcctgcgcctccctgcggctggacgtggc 120
 |||||
QY 121 TCTGACGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 |||||
Db 121 tctgacgacatcgctcgtcttcctgtaacttcgagcgacatggaatccaaagaaatcag 180
 |||||
QY 181 AAGACAGACTCACTGCTTTTATAGAAATCCGAGACTTCATGAAAGACAGATTTGACG 240
 |||||
Db 181 aagacagacactcaactgcttttatatagaatcctggaactccatgaaacagcagatltcagg 240
 |||||
QY 241 ACTGCACTCTGAGAGATGAAGACACACTACCTGACTCTCTGACGAGAGATGAACAGCCT 300
 |||||
Db 241 actgcaactctgagagatgaaagacacactacactgctcctcgaaggagatgaaacagcct 300
 |||||
QY 301 TTTCAGGGGCGCTGACAGAGAACTGCACACATTTGCGGCGCACAGCGCTTCTCAGAG 360
 |||||
Db 301 tttagggggcgctgacagagaaactgcacacatTTGCGGCGCACAGCGCTTCTCAGAG 360
 |||||
QY 361 CTCGACGTATGATGATGAAGCGCTCATGTTGATGCGCCGACGCGCAAGCGCTGAGCGCC 420
 |||||
Db 361 ctccagctatgatagaaagctcactggttgagatggtgcccagaggaagcctcgaagccc 420
 |||||
QY 421 AGCCATTTGCACACCTCAGCATCAATGCTGCGACATCCCATCGGTTCCCATAACTCA 480
 |||||
Db 421 agccatttgacacactcaacacatcaatgctgccaagcaccatcggttcccataaagtca 480
 |||||
QY 481 CTCGCTCCTGTTGGTTACAGATGAGCGCTGGCGCAAGATCTCTAATGACCTTAAGCA 540
 |||||
Db 481 ctccgctcctctggtacacagatcgaagcgcggcagaagatcctcaacatgacgttaagca 540
 |||||
QY 541 ACGGAACATGAAGGCTTAACCAAGATGGCTTCTTACTGTAAGCCCAATTTGCTTTC 600
 |||||
Db 541 acggaacacaaaggttaaccaaagatgctctctctacccgtgaagccaaatctgcttcc 600
 |||||
QY 601 GGCATCATGAACATCGCGGAAGCTACCTACAGACTTCTTACAGCTGATGCTGATGCTG 660
 |||||
Db 601 ggcatactgaacacatcgggaagcgtacactcaagactctctcagctgagtgtatgctcg 660
 |||||
QY 661 TTAAACACAGATCAAAATCCCAAGTCTCATAACTGATGAAGGAGGAGACAGCAAAA 720
 |||||
Db 661 ttaaacacagatcaaaatcccaagctctcatlaaccctgacgaaggaagacagaaa 720
 |||||
QY 721 ACTGCTGGGCAATTCGAATTCACATTTTATTCATAAATGTTGGGGATTTTTCAGC 780
 |||||
Db 721 actgctgggcaatctcgaaatctcaactcttaactcaaaatglttggggatttcttaagc 780
 |||||
QY 781 TCCGACGTGTAAGAAATTAAGATTAAGTGTCAACCTTCCCTGCTGATCCGATC 840
 |||||
Db 781 tccgagctgttgaaatlaagcatcaggltgtccaaaccttcctcgttgatccgagatc 840
 |||||
QY 841 AAGATGGAGATGCTTTGGGCTTTCAAGATCAGATCAGATGAGCTGATTCGTCG 900
 |||||
Db 841 aagatggagatgctttgggctttcaagatcagatcagatcagatcagatcagatcagatc 900
 |||||
QY 901 GAACATTAGCATGATGCTCTAGATGTTTGAANAATCTTTAAANAATGATGATGCTAT 960
 |||||
Db 901 gaacattagcatgattgctctagatglttggaactcttcaaaaatgltgltctat 960
 |||||
QY 961 ACATGTTAGATACATCAAGACATGCGCCACGAGTATGAACATCAGCCCTCTCTC 1020
 |||||
Db 961 acatglttaagactacaaagacatgcccacggtgttgaactacacagccctctctc 1020
 |||||
QY 1021 TTGAGCTGTACAGTTGTATATATGTAAGTCAATGATGATGATGATGATGATGAT 1080
 |||||
Db 1021 ttgagcctgtacagttgtatataatgtaagtcacatgagtgatgattcatcgtgtat 1080
 |||||

```

QY 1081 TACCAACGGTTTACATTTTGTATGATTTCTTACAGATTTGACAGATGGAGAGT 1140
    |||||||
Db 1081 taccacacgggtttaccatlttgaatgatttcttaagaattgaaccggattggagaggt 1140
QY 1141 ATTCCAGTCTTATGAAAACTTACACGTGAGCTATGAGGAGGGGTGACAGTCTCTGGGT 1200
    |||||||
Db 1141 attccgagtctatgaanaactacacgtgcatggaagggtcaccagtcctcgtggt 1200
QY 1201 CTACACCCCTGACACATGCGCCACTGAGAACCTTGAAATTAAGAGATGCGATGATGCA 1260
    |||||||
Db 1201 ctacaccttgacatgctgcacccctgagaaacctgaatlaagagatgcccattgcatgca 1260
QY 1261 AAGAAATGATGATGATGAGAGGATTAAGTTCTTTGAAATGTTACATTCGCGTGGACCTGC 1320
    |||||||
Db 1261 aagaaatgatatgttgaagggttaagttcttgaattgttaactatgctgcggagaccgc 1320
QY 1321 AAATTAAGTTCTTTTCTTAATGAGAGAGAGAAAAATATATATTTTATATTAATGCTTA 1380
    |||||||
Db 1321 aaataagttcttttcttaatgagagagaaaaataatatttataataatgtcta 1380
QY 1381 AAGTTATATTTACAGTGTAAATGTTTCTGTCGCAAGTTTGTAAATTTATTTGTCAT 1440
    |||||||
Db 1381 aagttatatttcagggttaatgatttctcgtgcaaaagtttgaattatattatgtgcata 1440
QY 1441 AGTATTTGATTCAAAAATTTTAAAAATGTCACATGATTAATTAATGTTTAAATG 1500
    |||||||
Db 1441 agtatttgattcaaatctttaaataatgctcactgtagcaataatttaatttaaatg 1500
QY 1501 TACAGATGATTTAACTGTCGACCTTTGTAATTCCTCGAAGGATCTGTGATGAGGG 1560
    |||||||
Db 1501 tacagatgattacttaactgctgcaacttgtaattccctgaagtaactgtagctaaagg 1560
QY 1561 GCAGATATCTGTTCTGTCGACACATGATTAATTTCTTATTTTAACTTATTA 1620
    |||||||
Db 1561 gcagataactgcttctcgtgacacacatgatttcttattcttctaacttaata 1620
QY 1621 GAGTCTTCAG 1630
    |||||||
Db 1621 gagtcttcag 1630

RESULT 3
AADI5310
ID AADI5310 standard; cDNA: 1630 BP.
XX
AC AADI5310;
XX
DT 15-NOV-2001 (first entry)
XX
DE Murine receptor activator of NF kappaB ligand (RANKL) cDNA.
XX
KW Murine: receptor activator of nuclear factor kappaB ligand; RANKL; NF;
KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW immune response; inflammatory response; graft-versus-host reaction;
KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory; ss.
XX
OS Mus musculus.
XX
Key Location/Qualifiers
FH 3..887
FT CDS
FT /*tag= a
FT /product= "Murine RANK ligand (RANKL) protein"
FT /note= "CDS does not include start codon"
FT /partial
FT
FT
PN US6271349-B1.
XX
PD 07-AUG-2001.
XX
PF 17-DEC-1998; 98US-0215649.
XX
PR 23-DEC-1996; 96US-0059978.

```

```

PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0772330.
PR 07-MAR-1997; 97US-0813509.
PR 22-DEC-1997; 97US-0996139.
XX
XX (IMMUNEX CORP.
XX
XX Dougall WC, Galibert L;
XX
XX WPI: 2001-52033/57.
XX
XX P-PSDB; AAE08737.
XX
XX New receptor activator of NF-kappaB (RANK) polypeptides, useful for
XX regulating immune response, in screening for RANK inhibitors, or as an
XX adjunct therapy for disease characterized by neoplastic cells that
XX express RANK
XX
XX Example 7; Column 63-66; 47pp; English.
XX
XX The patent discloses novel receptor activator of nuclear factor (NF)-
XX kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
XX of the tumour necrosis factor (TNF) receptor superfamily and associates
XX with TNF receptor associated factor (TRAF) 2 and 3 which are important
XX in the regulation of immune and inflammatory response. The receptors
XX are useful for regulating immune response and in screening for inhibitors
XX of these receptors. The cytoplasmic domain of RANK is used in developing
XX assays for inhibitors of signal transduction, e.g. for screening the
XX molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
XX TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
XX are useful in ameliorating the negative effects of an inflammatory
XX response that result from triggering of RANK, e.g. in treating toxic
XX shock or sepsis, graft-versus-host reactions, acute inflammatory
XX reactions and the effects of bone resorption. RANK acts as an anti-
XX apoptotic signal and rescue the cells that express RANK from apoptosis.
XX Soluble forms of the receptor are used in vivo or in vitro based
XX screening tests for agonists or antagonists of RANK activity, as
XX antagonists of RANK-mediated NF-kappa B activation, or to inhibit
XX transduction of a signal via RANK. RANK compositions are used in the
XX development of both agonistic and antagonistic antibodies, or as an
XX adjunct therapy for disease characterised by neoplastic cells that
XX express RANK. Compounds that interfere with RANK/TRAF6 interactions
XX are useful for modulating the formation of osteoclasts from osteoclast
XX precursors and for modulating osteoclast function and activities. They
XX are used as inhibitors of diseases associated with excess bone resorption
XX and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
XX useful for the expression of recombinant proteins, as probes for analysis
XX of the presence or distribution of RANK transcripts, while the proteins
XX are useful in preparing kits for the detection of soluble RANK, or
XX monitor RANK-related activity. The present sequence is a cDNA encoding
XX murine RANK ligand (RANKL) protein.
XX
XX Sequence 1630 BP: 436 A; 355 C; 379 G; 460 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 1630; DB 22; Length 1630;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1630; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCGGCGTCCCNACGAGGTCGCGACCCGCGGCTTGTGACAGGCTCGCGCGCCG 60
    |||||||
Db 1 ccggcggtcccaacagaggtccgcgcaccccggtcttgcacaggtctccggcgccg 60
QY 61 CACCGCGCGCTCCCGCTCCATGTTCTGTGCGCTTCTGAGGCTGGAGCTGGCGCAGGTGG 120
    |||||||
Db 61 caccgcgccgtcccgctcccatgttctgtgcttctgaggtctggagctggcgccaggtgg 120
QY 121 TCTGACGATGCGCTGTGTTCTGTACTTTGAGCGCAGATGATGATCTTACAGAAATATCAG 180
    |||||||
Db 121 tctgacgatgctgtgttctgtacttctgagcgagatgatatcttaacagaatatcag 180
QY 181 AAGACAGCAGCTACGCTTTTATAGATTCGTGAGCTCATGAAGCAGAGATTGGCAGG 240
    |||||||

```

```

Db 181 aagacgcacctcactgcttctabagaa tccctgagactcca tgaacgcagatcttgcaag 240
Oy 241 ACTCGACTCTGGAGAGTGAAGACACACTACTGACTCTGCTGAGAGAGTGAACAAAGCCT 300
Db 241 aactgcgactctgagagtgagaaacacactcctgactcctgcgagggagatgaaacaaagcct 300
Oy 301 TTCAGGGGGCCCTGCCAAGAAAGAACTGCACACATTTGTGGGGCCACAGCCCTTCTCAGAG 360
Db 301 tctcaaggggcgctgycagaaagaaactgcaacacatctgctgggccaacgcgctctcagag 360
Oy 361 CTCGACCTTGTGATGGAAGGCTCATGGTTGGATGTGGCCCGCAGGAGGAGCAAGCTGAGGCC 420
Db 361 cctcagcctctgctgagaaagctcactgctgagatgctgagccagagcaagccttgagcc 420
Oy 421 AGCCATTTTGCACACCTCACCATCAATGCTGCAGCATCCCATCGGGTTCCCTAAAGTCA 480
Db 421 agccatttgacacactcaccacacatctgcgcgacatcccatcgggttcccaataagctca 480
Oy 481 CTCTGCTCTTGTGTACCAAGATTCGAGGTGGGCCAAGATCTCTTAACATGACGTTAAGCA 540
Db 481 cctctgctcctctgctgacacgcagctcgaggtcgggccaagatctctaaactgaactga 540
Oy 541 ACGGAAACTAAGGTTAAACCAAGATGGCTTCTATTACCTGACGCCAACAATTTGCTTTC 600
Db 541 acggaaactaaagggtttaaaccagaatgctctctactaactctgaagccaacatctgcttc 600
Oy 601 GGCATCATGAAGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGTTATGTCG 660
Db 601 ggcatactaaacacacgcgaaagcgtacctaagactactcttaagctgctgctgatactgc 660
Oy 661 TTTAAACCGCATCAAAATCCCAAGTTCATTAACCTATGAAGAGAGGAGGACGAGAAA 720
Db 661 ttaaaacgcgcatacaaaatcccaagctctcctaaccctgaagaaaggagagacgaa 720
Oy 721 ACTGCTCGGGCAATTTCTGAATTTCCACTTTTATTCATTAATGTTGGGGATTTTTCAGC 780
Db 721 actgctcgggcaattctgaaattccactcttaactaaatgcttggggatcttctcaagc 780
Oy 781 TCCGAGCGTGTGAAGAAATTAGCATTCAGGTGTCACACCTTCCCTGCTGATCCGGATC 840
Db 781 tccgagcggtgtgaagaaattagcatctcaggtctcacaacccctcctgctgatacgcg 840
Oy 841 AAGATGCGAGCTACTTTTGGGCTTTCAAAGTTACAGAGCATAGCATGACACTATTTGCTG 900
Db 841 aagatgcgagctactcttggggcttccaagcttcaggaaatagatgaaacccaatctcg 900
Oy 901 GAACATTAGCATGATGCTCTAGATGTTTGAACCTTCTTAAAAAATGATGATGATCTAT 960
Db 901 gaacattagcatgagatgctcctagatgcttggaaactcttataaaatgagatgctat 960
Oy 961 ACATGCTTAAGACTACTTAAGAGACATGGCCACCGTGTATGAACCTCACAGCCCTCTCTC 1020
Db 961 acatgcttaagactacttaagagacatggccacgcgtgtatgaacctcacagccctctctc 1020
Oy 1021 TTGAGCCCTGTACAGTGTGTATATGTAAGTCCATAGATGATGATGATGATGATGAT 1080
Db 1021 ttgagccctgtacaggttgctgtatatagttaaaagtcataagtgatgattcatcagtgat 1080
Oy 1081 TACACACGCGTTTAAATTTTGTAAATGATTTCTTACAAATGAACAGATTTGGAGAGT 1140
Db 1081 tacacacgcgctttaaacttctgtaatgattccttagaatgaaacagatctggagaggt 1140
Oy 1141 ATTCCGATGCTTATGAATAAACTTACAGTGTGATGGAAGGGGTGACAGTCTCTGCTG 1200
Db 1141 attccgatgcttattgaataaaacttacagtgagctcagtggaagggggtcacagctctcctgg 1200
Oy 1201 CTAAACCCCTGGACATGTGCCACTGAGAACCTTGAATAATTAGAGAGATCCATGTCTATGCA 1260
Db 1201 ctaaaccccttgacaatgctgcactgagaaacttgaaatlaagagatgcatgctatgca 1260
Oy 1261 AAGAAATGATGATGCTGAAGGTTAACTTCTTTGTAATTTTACTTTGCGCTGGAGACTGC 1320
Db 1261 aagaaatgatatgctgaaagggttaagctcttctgtaattgtaactctgctgagacctgc 1320

```

```

Oy 1321 AAATAGTTCTTTTTTCTTATGAGAGAGAAATAATATGATTTTATATTAATGCTTA 1380
Db 1321 aaataagttcttttttcttatagagagagaaaaatatagtlatcttataataatgctta 1380
Oy 1381 AAGTTATTTTCAGGTGAATGTTTCTGTCGAAAGTTTGTAAATTAATTTGTGCTAT 1440
Db 1381 aagttatacttcaggtgataatgcttctctgctgcaaaagttctgtaaatcatatctgctat 1440
Oy 1441 AGTATTTATTTCAAAATATTTTAAAAATGCTCTACTGTTGACATATTTAATGTTTAAATG 1500
Db 1441 agtatttatacaaatattttaaataatgctcactgctgacatatataatcttcttaactaata 1500
Oy 1501 TACAGATGATTTTAACTGCTGACTTTGTATTTCCCTGGAAGTACTGTAAGCTTAATA 1560
Db 1501 tacagatgattttaaactgctgactttgttaattccctgaaagtaactcgtacgaagg 1560
Oy 1561 GCAGAAATACGTTTCTGCTGACACATGATAGTTATTTCTTTATTTCTTTTAACTTAATA 1620
Db 1561 gcagaaatactgcttctgctgacacatgatagttattcttcttacttcttcttaactaata 1620
Oy 1621 GAGTCTTCAG 1630
Db 1621 gagtcttcag 1630

```

```

RESULT 4
AAD08714
ID AAD08714 standard; cDNA; 1630 bp.
XX
AC AAD08714;
XX
DT 04-SEP-2001 (first entry)
XX
DE Murine receptor activator of NF- $\kappa$ B ligand (RANKL) cDNA.
XX
KW Murine; receptor activator of NF- $\kappa$ B; RANK; tumour necrosis factor;
KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KW chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein; ss.
XX
OS Mus musculus.
XX
FH Key 3..887 Location/Qualifiers
FT CDS
FT
FT /*tag= a
FT /product= "Murine RANKL protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN US6242213-B1.
XX
PD 05-JUN-2001.
XX
PE 22-DEC-1997; 97US-0995659.
XX
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
XX
PA (IMMUNEX ) IMMUNEX CORP.
XX
PI
XX
XX Anderson DM;
XX
XX WPI; 2001-407216/43.
XX
XX P-PSDB; AAE04425.
XX
XX New DNA molecules, useful for producing ligands (which are useful for
XX regulating immune response and in screening for inhibitors of NF- $\kappa$ B
XX receptor activator) of the receptor activator of NF- $\kappa$ B (RANK)
XX Example 7; Column 57-60; 43pp; English.
XX
XX The present invention relates to receptor activator of NF- $\kappa$ B (RANK)

```

CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular
CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
CC The ligands are useful for regulating immune response and in screening
CC for inhibitors of RANK. The present sequence is murine RANKL cDNA.
XX
XX
SQ Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 100.0%; Score 1630; DB 22; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCGGGTCCACAGAGAGGTCCTGACCCCGGCTTTCGACCGGCTCCGGCGCCG 60
    |||||||
Db 1 cggggtccacaagagaggtcgtgaccccgcttcgcaacggctcggcgccgc 60
QY 61 CACCGCGCCTCCCGCTCCATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
    |||||||
Db 61 caccgcgctcccgctcccaatgctcgtgctgctgctgctgctgctgctgctgctg 120
QY 121 TCTGAGCATGCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 180
    |||||||
Db 121 tctgagatcgctctgctcgtgctgctgctgctgctgctgctgctgctgctgctgctg 180
QY 181 AAGAGCAGCTACTGCTGTTTATAGAACTGAGACTCCATGAAAACGAGATTTCAGG 240
    |||||||
Db 181 aagagacagctactgctgtttatagaaactgagactccatgaaaacgagatttcag 240
QY 241 ACTGCATCTGGAGAGTGAAGACACACTGACTCCTGCGAGGAGTGAAGACAGCT 300
    |||||||
Db 241 actgcactctggagagtgaaagacacactgactcctgcaaggagtgaaacagcct 300
QY 301 TTCAGGGGCGCTGCGAGAGAACTGAACTGTTGGGCGCACAGGCTTCTCAGAG 360
    |||||||
Db 301 ttcaggggcgctgcgagagaaactgaaactgcaacattgtgggccaagcctctcagag 360
QY 361 CTCGAGTATGATGAAAGGCTCATGTTGATGTTGATGTTGATGTTGATGTTGATG 420
    |||||||
Db 361 ctcgagtatgataagagctcatggttgatggttgatggttgatggttgatggttgatg 420
QY 421 AACCATTTCACACCTACACATCAATGCGCAGACATCCATCGGTTCCATAAGTCA 480
    |||||||
Db 421 aaccatttcacacctacacatcaatgcgacagatcccatcggttccataagtgca 480
QY 481 CTCTGCTCTTGTGTACGACGATCGAGGCTGGCCAAAGATCTCTAATGACGTTAAGCA 540
    |||||||
Db 481 ctctgctcttgtgtacgacgatcgaggtggccaaagatctctaattgacgtttaagca 540
QY 541 ACGGAAACTAAGGTTAAACCAAGATGCGTTCTATTACTGTACGCAATTTGCTTTC 600
    |||||||
Db 541 acggaaactaagggttaaaccaagatgcggttctattactgtacgcaatttgcttcttc 600
QY 601 GGCATGATGAACATCGGAGAGGCTACTACAGACTATCTTACGCTGATGCTGATGCTG 660
    |||||||
Db 601 ggcataatgaacatcggagaggtactactacagactatcttcgctgctgctgctgctg 660
QY 661 TTAACAACGACATCAAAATCCAAAGTTCTCATTAACCTGATGAAGAAGAGACACAAA 720
    |||||||
Db 661 ttaaacacgacatcaaaatccaaagtctcatataacctgataagagaggaagcaaaaa 720
QY 721 ACTGTCGGGCAATTTCTGAATTTCCATTTTATTCATAATGTTGGGGGATTTTCAAGC 780
    |||||||
Db 721 actgtcgggcaatttctgaatttccattttatttccataaattgttggggattttcaagc 780
QY 781 TCCGAGCTGGTGAAGAATAATGATTCAGGTGTCACAACTTCCCTGCTGATCCGATC 840
    |||||||
Db 781 tccgagctggtgaagaataatgattcaggtgtgccaaaccttccctgctgctgctgctg 840
QY 841 AAGATGCGAGCTACTTTGGGGCTTTCAAAAGTTCAAGACATAGACTCAITTCGTG 900
```

```
Db 841 aagatgagcagctactctgggtcttcaagttcagagacatagactgagactcattcgag 900
    |||||||
QY 901 GAACATTAGATGAGATGCTCCTAGATGTTGGAAACCTTTAAAAATGATGATGCTAT 960
    |||||||
Db 901 gaacattagatgagatgctcctagatgttggaaacctttaaataatgatgagtgctat 960
QY 961 ACATGTTAGACTACTAAGAGACATGAGCCACGAGTGTATGAACCTCACAGCCCTCTC 1020
    |||||||
Db 961 acatgttaagactactaagagacatgagccacagtgatgaactcaacagccctctc 1020
QY 1021 TTGAGCTGTACAGGTTGTATATGTAAGTCCATAGCTGATGATGATGATGATGAT 1080
    |||||||
Db 1021 ttgagctgtacaggttgtataltgtaaagttccatagtgatgagatcctagtgat 1080
QY 1081 TACACAGGCTTTTACAAATTTTGAATGATTTCTAGCAATTTGAACAGATTTGGAGAGT 1140
    |||||||
Db 1081 tacacaggttltacaaatlttgaatgatttctagaaatltgaacagatltggagagtg 1140
QY 1141 ATTCCGATGCTTATGAAGAACTTACACAGTACGCTATGGAAGGGGCTCACAGTCTG 1200
    |||||||
Db 1141 attccgattgtatgaaacttacacagtgatgaaagggttcacagctcttggt 1200
QY 1201 CTAAACCCCTGACATGTCGCCACTGAGAACTTGAAATTAGAGAGATGCAATGCA 1260
    |||||||
Db 1201 ctaaaccttgacatlgcaccactgagaaacctgaaatlaagagagatgcatgtcatgca 1260
QY 1261 AAGAAATGATGATGTAAGGCTTAAGTTCTTTGAAATTTGTACATTCGCTGGACCTGC 1320
    |||||||
Db 1261 aagaaatgatgatgtgaaggcttaagttctttgaaatgtgtacatctgctggacctgc 1320
QY 1321 AAATTAAGTTCTTTTCTAATGAGAGAGAGAAAAATATATGATTTTATATATGCTA 1380
    |||||||
Db 1321 aataaagttcttttctaaatgagagagaaaaatataatgtatttataatgctca 1380
QY 1381 AAGTTATTTTCAGTGTAAATGTTTCTGTCGCAAGTTTGTAAATATATTTGCTAT 1440
    |||||||
Db 1381 aagttataatcagtgtaagtttctgcaagtttgttaataatataatlttgctat 1440
QY 1441 AGTATTTGATTCAAAAATTTTAAATGTCACAGTGTGACATATTTAATGTTTAAATG 1500
    |||||||
Db 1441 agtatttgatccaataatlttaaaaatgtctcactgtgacatalttaattttaaag 1500
QY 1501 TACAGATGATTTTAACTGTCGACTTTGATTTCCCTGGAAGTACGCTGATGAGGG 1560
    |||||||
Db 1501 tacagatgattttaaactgtgacacttgaatccctggaagtgactcgtgacaaagg 1560
QY 1561 GCAGATATCTGTTCTGCTGACACATGATGTTATTTCTTTTACTTAATA 1620
    |||||||
Db 1561 gcagatatctgttctgtgacacatgatttttcttttactttaata 1620
QY 1621 GAGTCTTCAG 1630
    |||||||
Db 1621 gagtcttcag 1630
```

RESULT 5
AAD05903
ID AAD05903 standard; cDNA; 1630 BP.

AC AAD05903;

DT 31-JUL-2001 (first entry)

XX

DE Murine RANKL (receptor activator of NF-kappaB ligand) cDNA.

XX

KW Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;

XX

KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;

KW

KW TNF receptor associated factor; TRAF; RANK ligand; RANKL; osteopathic;

KW

KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;

KW

KW immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; Ep; cytostatic; ss.

OS	Mus musculus.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	3..887
FT		/*tag- a
FT		/product- "Murine RANKL (receptor activator of
FT		NF-kappaB ligand) protein"
XX		
PN	MO200136637-A1.	
XX		
PD	25-MAY-2001.	
XX		
PP	14-NOV-2000; 2000MO-US31459.	
XX		
PR	17-NOV-1999; 99US-0442029.	
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Anderson DM, Hughes AE;	
XX		
DR	WPI; 2001-329222/34.	
DR	P-PSDB; AAEO1992.	

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX
PS Example 7; Page 72-74; 96pp; English.

Example 7: Page 72-74; 96pp; English.

CC The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a type I
CC transmembrane protein that interacts with TNF receptor-associated
CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
CC of the transcription factor NF-kappaB, a ubiquitous transcription factor
CC that is most extensively utilized in cells of the immune system.
CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
CC negative effects of inflammatory reactions, and the effects of excess
CC bone resorption. The RANK DNAs, proteins and their analogues are useful
CC for the preparation of pharmaceutical compositions, for infecting target
CC cells for use in gene therapy applications in diagnosing diseases
CC associated with RANK, and as targets for use in screening assays. They
CC may be used in the treatment or diagnosis of immune system dysfunction.
CC The present invention also encompasses gene therapy methods to correct
CC gene-activating mutations, associated with e.g. familial expansile
CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present sequence is a cDNA encoding murine RANKL (murRANKL) protein.
XX

Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match	100.0%	Score 1630;	DB 22;	Length 1630;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1630; Conservative	0;	Mismatches	0;	Gaps 0;

0Y	1	CGGGGCTCCACACAGAGAGGTCGGCTGGACCCCGCGCTTTCTGACACGGGCTCCGGCGCCG	60
Db	1	ccggcgcccccacacagagggctccgcctgcaccccgcccttcgcaccggtcccgcgccgc	60
0Y	61	CACCCGCCGCTCCCGCTCCATGTTCTCTGGGCGCTCTGGGGGCTTGAGCTGGGCGAGGTG	120
Db	61	caccgcgcgcctcccgctccacatgtctcttgcgcctctgggacctggagcttgycacagttg	120
0Y	121	TCTGCAGCATGCTCTGTCTCTGACTTTCGAGGCGGAGTGGATCCCTAACAGAAATACG	180
Db	121	tctgcagatctgcctgtctctgtaccttcgagagcagatgagatcccaacagatatcag	180
0Y	181	AAGCAGCAGCTCACTGCTTTTATAGAATCCGAGACCTCATGAAACGCGAGATTGCAGG	240
Db	181	aagcagagacactcgtcttcttatgaatcccgagaccatcaagaaacgcagatttgcag	240
0Y	241	ACTGCAGCTCTGGAGAGTGAACACACACTTACCTGACTCTCGAGAGGATGAAACAAGCCT	300

Db	241	actgcgactctcgtgagatgtagaagacacactaccctgaactctctcgtcagagagatgtaaacaaagcct	300
Oy	301	TTCAAGGGGCGGTGCAGAGAAGAACTGCACACACATTTGTGGGGGCCACAGCGCTTCTCAGAG	360
Db	301	ctcaaggggcccgtgcagaaaggaactgtacaacatctgtggggccaacagcgctctctcaagg	360
Oy	361	CTCCAGCTATATGGAAGGCTCATGGTTGGATGTGGCCACGCGAGCGAAGCCTGAGGCC	420
Db	361	ctccagctatgtagaagagctcactgtgtgtagtctggcccagcgaggcaagccctgagccc	420
Oy	421	AGCCATTTGGCACACTCTCACCATCAATCTCTCCAGCAATCCCATCGGGTTCGCCATTAAGTA	480
Db	421	agccatttgcacacctcaccaaccaacgctgcgcagacccaacgcgtctccctaaggtca	480
Oy	481	CTGTGCTCTTGTGGTACACAGATCGAGGCTGGGGCCAAAGATCTTAACTATGACGTTTAAGCA	540
Db	481	ctctgtcctctctgtctaccacgactcgagcgctgggcgaagatctcttaacatgtaagcttaagca	540
Oy	541	ACGGAACACTAAGGGTTAACCAGATGCGCTTCTTAATTAACCTGAACGCCAACATTTGCTTTC	600
Db	541	acggaaacactaaggcttcaacacagatgctctctatctaacctgctcgcacaacatctgcttc	600
Oy	601	GGCATTCATGAACATTCGGGAAAGCGCTACTCTACACACTATCTTCAGCGATGGGTATGTCG	660
Db	601	ggcatcatgaaacatcgcgggaagcgtctaccctcaagactctctccagctggaagtgtatgtcg	660
Oy	661	TTTAAACACGAGCATCMAAATCCCAAGTCTCTCATTAACCTGATGAAGAGGAGGACACAGAAA	720
Db	661	ttaaacacagatcaaaaaatcccaagctctctatacctctgataaaggaagggagcaagaaaa	720
Oy	721	ACTGCTGGGCAATTCGAAATTCACACTTTTAAATTCACATAAATGTTGGGGATTTTTCACAC	780
Db	721	actgctggggcaattctcgaaatctccactcttattccataaagtctggggatcttctcaagc	780
Oy	781	TCCGAGCGGGGAAGAAATTAAGCATTAAGTGGTGCMAACCTTCCCGTCGCGMATCCGGATC	840
Db	781	tccgagcggggaagaaatctagactctcaagctgctcaaacctctcccgctggatccggatc	840
Oy	841	AAGATGGACGCTACTTTTGGGGCTTTCMAAATTCAGACATAGACTGAGACTCATTTTCGTG	900
Db	841	aagatggacgctactcttggggccttccaagctcaggaacataagctctgagctctcttcgtg	900
Oy	901	GAACTATTAAGCATGGAATGCTCAGATGTTTGGAACCTTCTTAAATAATGATGATGTCAT	960
Db	901	gaactattagactgtagtctctctagatgtcttgaaacctcttaaaaaatgtagtgcata	960
Oy	961	ACATGTGTAAGACTCAATAGAGGAGCATGGGCCAGGGGTATGAACATCACAAGCCCTCTCTC	1020
Db	961	acatgtgtaagactcaatagagagacatgcccacggtgtctagaaacctcaagacctctctc	1020
Oy	1021	TTGAGCCTGTACAGTGTGTATATATGAAGTCCATAGGAGATGTAAAGATTTAGTGTGAT	1080
Db	1021	ttgagcctgtacagtgctgtgctatctgtaaaagtccaaatgagtgtatgattcaatgtagtgc	1080
Oy	1081	TACACAACGGTTTTACAAATTTGTGAATGATTTCTAGAAATTGAAACCGAGATTGGAGAGGT	1140
Db	1081	tacacaacggttttacaactttgaaatgattctcctaagaatttgaaacagatctgggagaggt	1140
Oy	1141	ATTCCGAGTCCTTAATGAAGAACTTAACACGTGAGCTATAGGAAGGGGGTCAACAGTCTGGGT	1200
Db	1141	attccgagctcttaagaaacacttaccacgtgtagcttagaaggggggtccacagctctcggct	1200
Oy	1201	CTAACCCCTGACATATGAGCCACTGAGAACTTGAATTAAGAGAGATGCCATGCAATTTGGA	1260
Db	1201	ctaacccctgacatctgtgcacactgagaaaccttgaatatgaaggaatgcaatgcatatgta	1260
Oy	1261	AAGAAATGATAGTGTGAAGGCTTAAAGTCTTTTGAATTTGTTACATTTGCCCTGGACCTGC	1320
Db	1261	aagaaatgatagtgtagaaggtctaaagttcttgtaattgttaacatctgcctgaggacctgc	1320
Oy	1321	AAATTAAGTCTTTTTTCTTAATGAGAGAGAAAATATATATATTTTATATATGTCTA	1380
Db	1321	aaataaagttcttttcttctaagaggaagaaaaataatgtaattcttctaataaagttcta	1380

QY 1381 AACGTATATTTCAGTGTAAATGTTTCTGTCAGCAAGTTTGTAAATTAATATTTGCTAT 1440
CC |1381| aagttatatttcagggtgaaagtttcggtgcaagtttgtaatacatatttgcgtat 1440
Db 1381 aagttatatttcagggtgaaagtttcggtgcaagtttgtaatacatatttgcgtat 1440
QY 1441 AGATTTCATTCACAAATATTTAAATATGTCACCTGTTGACATATTTAATGTTTAAATG 1500
CC |1441| agttttgattcacaataatatttaaaatgcttcactgttgacataatttaattttaaag 1500
Db 1441 agttttgattcacaataatatttaaaatgcttcactgttgacataatttaattttaaag 1500
QY 1501 TACAGATGATTTTAACTGCTGACCTTTGTAATTCCTCGAAGGTACTGCTAAGGGG 1560
CC |1501| tacagatgattttaaactggtgactttgtaattccctgaaggtactgctgaaggg 1560
Db 1501 tacagatgattttaaactggtgactttgtaattccctgaaggtactgctgaaggg 1560
QY 1561 GCAGATACCTGTTCTGTCGACACATGATTAATTTCTTATTTTAACTTAATA 1620
CC |1561| gcagataactggttcctggtgacacatgatttattcttattctttaaacttaata 1620
Db 1561 gcagataactggttcctggtgacacatgatttattcttattctttaaacttaata 1620
QY 1621 GAGTCTTCAG 1630
CC |1621| gagtcttcag 1630
Db 1621 gagtcttcag 1630

RESULT 6
AAV70284
ID AAV70284 standard; DNA; 2295 BP.
XX
AC AAV70284:
DT 11-FEB-1999 (first entry)
DE Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins.
XX
KW Human: osteoprotegerin binding protein; OPG binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 158..1108
FT /tag= a
FT /product= "osteoprotegerin binding protein"
XX
PN W09846751-A1.
XX
PD 22-OCT-1998.
XX
PF 15-APR-1998; 98WO-US07584.
XX
PR 30-MAR-1998; 98US-0052521.
PR 16-APR-1997; 97US-0842842.
PR 23-JUN-1997; 97US-0880855.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle MJ;
XX
DR WPI: 1998-594578/50.
DR P-PSDB; AAM83194.
XX
PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX
PS Claim 1; Fig 1; 47pp; English.
CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OPG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including

CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.

SQ Sequence 2295 BP; 648 A; 487 C; 538 G; 622 T; 0 other:

Query Match 99.9%; Score 1628.4; DB 19; Length 2295;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGCTCCACACAGAGGGTCCGCTGCACCCCGGCTTCGTGACCGGGCTCCGGCGCCG 60
CC |1| cccggctccacacagaggggtccgctgcaccccggttcgtgacccggctccggcgccg 60
Db 222 ccggctccacacagaggggtccgctgcaccccggttcgtgacccggctccggcgccg 281
QY 61 CACCGCGCCCTCCCGCTCCATGTTCTGCGCCCTCTGCGGCTGGGACTGGGCGCAGTGG 120
CC |61| caccgcgccctcccgctccatgttctgcgccctctgcgggctgggactgggcgacagtgg 120
Db 282 caccgcgccctcccgctccatgttctgcgccctctgcgggactgggactgggcaagtg 341
QY 121 TCTGCAGCATGCGCTGTCCTGCTGATCTTTCGAGCGCAGCATGATCTTAAAGAAATATCAG 180
CC |121| tctgcagcatgctgctgtctgctgatttctgagcgcgagcatgattcttaagaaatattcag 180
Db 342 tctgcagcatgctgctgtctgctgatttctgagcgcgagcatgattcttaagaaatattcag 401
QY 181 AAGACGACACTCAGTCTTTTATAGAACTCTGAGACTCCATGAAAGCGACATTTGACGG 240
CC |181| aagacgacactcagtcttttatagaaactctgagactcccatgaaagcgacattttgacgg 240
Db 402 aagacgacactcagtcttttatagaaactctgagactcccatgaaagcgactttgacgg 461
QY 241 ACTGCATCTGAGAGGTAAAGACACACTGATCTGATCTGAGAGGATGAACAGGCT 300
CC |241| actgcacttgagaggtaaagacacactgattctgattctgagagggatgaacaggct 300
Db 521 actgcacttgagaggtaaagacacactgattctgagagggatgaacaggct 521
QY 462 actgcacttgagaggtaaagacacactgattctgagagggatgaacaggct 521
CC |462| actgcacttgagaggtaaagacacactgattctgagagggatgaacaggct 521
Db 522 ttcagggggccgctgcagagaggaactgcgaacacattgttggccaaagctcttcaggag 581
QY 301 TTTGAGGGGCGCTGCAGAGGAAGTCAACATGTTGGGCGCACAGCGCTTCTCAGGAG 360
CC |301| tttagggggcgctgcagagaggaagtcaaacattgttgggcgcacagcgcttctcaggag 360
Db 582 ttcagggggcgctgcagagaggaactgcgaacacattgttggccaaagctcttcaggag 581
QY 361 CTCCAGCTATGATGGAAGGCTCATGTTGATGTGGCCACGACGAAAGCTTAGGCC 420
CC |361| ctccagctatgatggaaaggctcatgttgatgtggccacgacgaaagcttagggcc 420
Db 641 ctccagctatgatggaaaggctcatgttgatgtggccacgacgaaagcttagggcc 641
QY 421 AGCCATTGTCACACTCCACATCATGCTGCGAGATCCGATCGGGTTCCCTAAAGTCA 480
CC |421| agccattgtcacactccacatcatgctgcgagatccgatcgggttccctaaagtca 480
Db 701 agccattgtcacactccacatcatgctgcgagatccgatcgggttccctaaagtca 701
QY 481 CTTCTGCTCTTGGTACACGATCGAGGCTGGCCAAAGATCTCTAAACATGACGTTAAGCA 540
CC |481| cttctgctcttggtagcacgattcgaggctggccaaagattctctaaacattgacgtttaagca 540
Db 762 cttctgctcttggtagcacgattcgaggctggccaaagattctctaaacattgacgtttaagca 761
QY 541 ACGGAAATCTAAGGTTTAAACAAGATGCTTATTAATCTGATGACGCAACATTTGCTTC 600
CC |541| acggaaatctaaaggtttaaacaaagattgatttaattactgacgcaaacatttgccttc 600
Db 821 acggaaatctaaaggtttaaacaaagattgatttaattactgacgcaaacatttgccttc 821
QY 601 GGCATCATTAACATTCGGAAGCGTACCTACGACATTCCTAGCGGATGGTGTATGTCG 660
CC |601| ggcattcatataacatctcggaagcgtagcctacgacattcctagcggttggtgtatgtcg 660
Db 882 ggcattcatataacatctcggaagcgtagcctacgacattcctagcggttggtgtatgtcg 881
QY 661 TTTAAACAGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGCAGCAAAA 720
CC |661| tttaaacagacatcaaaatcccaagttctcatataactgattgaagagagcagcaaaaa 720
Db 941 tttaaacagacatcaaaatcccaagttctcatataactgattgaagagagcagcaaaaa 941
QY 721 ACTGATCGGGCAATTCGTGAATTCATTTTATTCATTAATGTTGGGGATTTTCAACG 780
CC |721| actgatcgggcaatttcgtgaatttcatttttatttcattcaataatgttggggaattttcaacg 780
Db 942 actgatcgggcaatttcgtgaatttcatttttatttcattcaataatgttggggaattttcaacg 1001

```

Oy 781 TCCGAGCTGTGTAAGAAATTACATTACAGGTCTCCACCCCTCCCTGCTGATCCGGATC 840
    |||
Db 1002 tcggagcttggtaaaataatagcaggtgtccaacctccctcgtcgtccggtc 1061
Oy 841 AAGATGCGACGACTTTGGGCTTCAAAAGTTGAGAGATAGACGACATCATTTCTGTG 900
    |||
Db 1062 aagagcgagcagcacttctgggcttccaaagttcagaaacatagacatgagactatctcg 1121
Oy 901 GAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
    |||
Db 1122 gaacattagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1181
Oy 961 ACATGTGTAGAGCTACTAGAGACATGGCCACGCTGATGAACTCAGACCCCTCTCTC 1020
    |||
Db 1182 acatgtgtagagcactactaagagacatggccacggtgtatgaaactcagacccctctc 1241
Oy 1021 TTGACCCGTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
    |||
Db 1242 ttgagccgtacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1301
Oy 1081 TACACACGCGTTTACAAATTTTGTATGATTTCTAGATTTGAAACACAGATTGGAGAGGT 1140
    |||
Db 1302 tacacacggtttacaaatttctgtaagtattcctagaaattgaaacagattggagaggt 1361
Oy 1141 ATTCCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGCTCAGCTCTGGGT 1200
    |||
Db 1362 attccgagcttcttgaataaacttacacgtgagcagcagcagcagcagcagcagcagcag 1421
Oy 1201 CTAAACCCCTGGACATGCTCCACTGAGACCTTGAATTAAGAGATGGCATGTCATGCA 1260
    |||
Db 1422 ctaaaccttgagacatgtgtccactggaaccttgaaatcaagagatgacatgtgca 1481
Oy 1261 AAGAAATATAGTGTGAAGGTTAAGTTCTTTGAAATGTTACATTGGCTGGGACCTGC 1320
    |||
Db 1482 aagaaatagatgtggaaggttgaagttcttctgtaattgttaacttgcgtggagaccgc 1541
Oy 1321 AAATAGTCTTTTCTTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
    |||
Db 1542 aaataagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1601
Oy 1381 AAGTATATTTTACAGTGAATGTTTCTGTCGCAAGTTTGTAAATTTATTTGAGCTAT 1440
    |||
Db 1602 aagtaatacttcaggtgaaagttcttctgcaaaagtttcttcttcttcttcttcttctt 1661
Oy 1441 AGTATTTATTTCAAAATATTTTAAATGCTCAGCTGTGACATATTTAATGTTTAAATG 1500
    |||
Db 1662 agtattcttcaaaaatacttcaaaaatgtctcactgtgacatacttaagtcttctaa 1721
Oy 1501 TACGATGATTTTAACTGTCGACCTTTGATTTCCCTGGAAGTACATGCTAAGGGG 1560
    |||
Db 1722 tacgagatcttcaactcgtgcaacttctgtaattccctcgaaagctcgtgctaaagg 1781
Oy 1561 GCAGAAATCTGTTCTGTGTCAGCAGATGATGATGATGATGATGATGATGATGATGAT 1620
    |||
Db 1782 gcagaaatctgttctcgtgacacatgtagttcttcttcttcttcttcttcttcttct 1841
Oy 1621 GAGCTCTTACG 1630
    |||
Db 1842 gagctctcag 1851

```

```

RESULT 7
AA299966
ID AA299966 standard; DNA: 2299 BP.
XX
AC AA299966;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a murine osteoprotegerin ligand (OPGL).
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KM tumour necrosis factor receptor; type II transmembrane protein;

```

```

KW osteoclast differentiation; CSF-1; osteoclast activator;
KM immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 170..1120
FT /tag= a
FT /product= "osteoprotegerin ligand"
XX
PN M0200015807-A1.
XX
PD 23-MAR-2000.
XX
PE 13-SEP-1999; 99MO-DK00481.
XX
PR 15-SEP-1998; 98DK-0001164.
PR 02-OCT-1998; 98US-0102896.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Haaning J;
XX
DR WPI: 2000-271444/23.
DR P-PSDB; AAY84419.
XX
PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT to treat, prevent and ameliorate osteoporosis -
XX
PS Disclosure; Page 82-85; 110pp; English.
XX
CC The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
SQ Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;

```

```

Query Match 99.9%; Score 1628.4; DB 21; Length 2299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 CGCGGCTCCACACAGAGGTCGCCGTGACCCGCGCTTCTGACCGCGCTCGGCCCG 60
    |||
Db 234 cggcggtccacacagaggggtccgtgaccccgcttctgacccggtccggtccggtccg 293
Oy 61 CACCGCGCGCTCCGCTGATGTTCTGCGCTGCGGGGCGGAGCTGAGCGGCGAGTGG 120
    |||
Db 294 caccgctcgctccgctccatgttccgtgctccctcggtgagcggagcggaggtg 353
Oy 121 TCTGACGATGCTGCTGTTCTGTTCTGATTTGAGCGCAGATGATGATGATGATGATGATGAT 180
    |||
Db 354 tctgacatgctgtctgttctgttctgttctgttctgttctgttctgttctgttctgttctgt 413
Oy 181 AAGACAGCATCTACTGTTTATAGATCTGTGAGATCCATGAAACGACGATTTGCGAG 240
    |||
Db 414 aagacagcatctactgttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 473
Oy 241 ACTGCACTGTGAGAGTGAAGACACTACTGCTGCTGACGAGAGAGAGAGAGAGAGAGAGAG 300
    |||
Db 474 actgcactgtgagagtgaagacactactactgtcttccgtcagagagagatgaaacagacct 533

```



```

OY 301 TTTCAGGGGCGCGTGCAGAGAACTGCACACATTGTGGGGCCACAGCGCTTCAGAG 360
Db 534 ttcaggggcccgtgcagaaagaaactgcacacattcgtggggccacagcgcttcacagag 593
OY 361 CTCAGATGATGAGAGGCTCATGTGGATGTGGCCCAAGCGAGGCAAGCCTGAGGCC 420
Db 594 ctccagatagatgagagggctcatggttggtggtggccagcgaggaagctgaagccc 653
OY 421 AGCATTGTCACACCTCCACATCAATGCTGCACATCCATCGGGTCCATTAAGTCA 480
Db 654 agccatttgcacacctcaacccaatcgtgcagcatcccaatcggttccataaagca 713
OY 481 CTCGTCTCTTGTGACAGATGAGGCTGGGCCAAGATCTCAACATGACGTTAAGCA 540
Db 714 ctctgtcctctgtgacacagatcgaggtcggtgccaagatctcaacatgscgtlaagca 773
OY 541 ACGGAAACCTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTC 600
Db 774 acggaaaactaagggttaaccagaagtgcttctattacatcgtacgccaacattgcttc 833
OY 601 GGCATCATGAAACATCGGGAAGCGTACTACAGACTATCTCAGCTGATGGTATGTCG 660
Db 834 ggcatacatgaaacatcggaaagcgactacagactatctcaagctgagtgatgctg 893
OY 661 TTAATAACAGCATCAAAATCCCAAGTTCATTAACCTGATGAAAGAGAGACAGAA 720
Db 894 ttaaaacagcatcaaaatcccaagttctcataaacttgatgaagagaggggcaagaaaa 953
OY 721 ACTGGTCGGGCAATTCTGAATTCACCTTTATTCATTAATGTTGGGATTTTCAAGC 780
Db 954 actgttcgggcaattctgaattccacttattcatalaattgttggtggtatlttcaagc 1013
OY 781 TCCGAGCTGCTAATAAATTACATTCAGTGTCCAACTCCCTCGTGGATCCGATC 840
Db 1014 tccgagctgtgtaagaaatlagcatcaggtgtccaaacctccctcggtgcggatc 1073
OY 841 AAGATGCGACGTACTTGGGGCTTTCAAAGTTCCAGAGACATAGACTGAGACTATTCTG 900
Db 1074 aagatgacgacgtacttggggcttccaaagttccaaagttcagactagacgtacatctcg 1133
OY 901 GAACATTAGCATGATGTCCTTGATGTTGGAACTCTTTAAATAATGATATGTCAT 960
Db 1134 gaacattagcatgattgtctcgtatgttgtaaaccttctaataatgtagtgcata 1193
OY 961 ACATGTGTAGACTACTAGAGACATGCGCCAGGCTGTGAACCTCAACAGCCCTCTCTC 1020
Db 1194 acatgtgtagactactactaagaacatgcccagtggtatgaactcaagccctctctc 1253
OY 1021 TTGAGCCTGTACAGTTGTGTATGTATGTAAGTCCATAGGTGATGTATCATGGTAT 1080
Db 1254 ttgagcctgtacaggtgtgtatgtatgtaagttccatagtgatgtatcatggtat 1313
OY 1081 TACACAAGCGTTTACAATTTTGTATGATTTCTTGAAATGACAGATTGGGAGAGGT 1140
Db 1314 tacacaagcgtttacaatttgtatgatttccatgaattgaccagattgggagaggt 1373
OY 1141 ATTCGATGCTTATGAAAACTACACGTGAGTATGGAAGGGGTCACAGTCTCGGGT 1200
Db 1374 attcgatgcttatagaaaaactacacgtgagctatggaaggggtcacagctctcggt 1433
OY 1201 CTAACCCCTGACATGTGCACATGAGAACCTGAAATTAAGAGATGCCATGTCTATGCA 1260
Db 1434 ctacccctgacatgtgcacatgagaaacttgaatlaagagatgacctgcatgtca 1493
OY 1261 AAGAAATGATAGTGAAGGGTTAAGTTCTTTGAATGTGTAATGTCGCTGGACCTGC 1320
Db 1494 aagaatgatagtgtaaggggttaagttctttgaaattgtaacatgctgtggacctgc 1553
OY 1321 AATTAAGTCTCTTTTCTAATGAGAGAGAAATATATGATTTTATATATGCTTA 1380
Db 1554 aataagttcttcttcttaatgagagagaaaaataatagatttttataataatgtcta 1613
OY 1381 AAGTTATATTCAGTGTAATGTTTCTGTGCAAAAGTTTGTAAATTAATATTTGTCTAT 1440

```

```

Db 1614 aagttatattcaggtgtaatgtttctgtgcagaagtttgttaataatattgtgctat 1673
OY 1441 AGTATTGATTCAAAATATTAAATAATGTCACCTGTGACATATTAAATGTTTAAATG 1500
Db 1674 agtattgtatccaataatlaataaatgtctcatcgttgcacatatttaagtttaag 1733
OY 1501 TACAGATGATTTTAACGTGTCACCTTTGTAATTCCTCTGAAGGACTCGTAGAGGG 1560
Db 1734 taacagatattttaactggtgacattgttaattccctgaaaggtactcgtagctaa 1793
OY 1561 GCAGAAATACGTGTTCTGTGACCAACATGTAATTTCTTATTTCTTTAACTTAATA 1620
Db 1794 gcagaatactgttctgtgtaaccaatgtagttattcttattcttattcttaactaata 1853
OY 1621 GAGCTTCACG 1630
Db 1854 gagcttcacg 1863

```

RESULT 8

AAV41489 ID AAV41489 standard; cDNA; 2191 BP.

AC AAV41489;

DT 24-SEP-1998 (first entry)

DE Nucleotide sequence of mouse 499E9 gene.

XX Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;

KW antagonist; autoimmune disorder; rheumatoid arthritis;

KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;

KW acute inflammatory response; antibody; antigen; cancer; ss.

XX Mus sp.

XX Key Location/Qualifiers

FH CDS 125..1072

FT /tag= a /product= "mouse 499E9 protein"

XX WO9825958-A2.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-US22766.

XX 13-DEC-1996; 96US-0032846.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Mattson JD;

XX MPI: 1998-348452/30.

XX P-PSDB: AAW59654.

XX Mouse cell surface antigen, 499E9 protein - used to treat conditions

XX associated with abnormal physiology or development

XX Claim 4; Pages 8-11; 59pp; English.

PS This is the nucleotide sequence encoding the mouse 499E9 protein, used
 CC in the method of the invention to treat conditions associated with
 CC abnormal physiology or development. The 499E9 protein is expressed
 CC highly on polarised Th1 T cells, binding of 499E9 to its receptor may
 CC result in either immune cell expansion or apoptosis. Antagonists of
 CC 499E9 may be used to modulate immune responses in abnormal situations,
 CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
 CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
 CC acute inflammatory responses in which T-cell expansion, activation or
 CC immunological T-cell memory play an important role. The antibodies
 CC can be used to raise anti-idiotypic antibodies which will be useful

SQ Sequence 2191 BP; 605 A; 461 C; 518 G; 607 T; 0 other;

Oy 1 CCGGCGTCCACACAGAGGGTCCGCTGCACC GCCCGGCCCTTTGTGCACGGCGCTCCGGCGCCG 60
|||||
Dd 189 ccgcgctccacacagagggtcgcgctgcaccgcccgccctctgcaccggctccgcggcgccgc 248
|||||

[illegible]

OY 1560 GGCAGAACTACTGTTCTGTCGACACATGATTATTCTTTTACTTAAT 1619
|||||
DB 1763 ggcaagatactctctctcgtgcacacatgtagttcattcttcttcttaactaat 1822
|||
OY 1620 AGAGCTCTCAG 1630
|||||
DB 1823 agagctctcag 1833
|||
RESULT 10
AAV69886 standard: cDNA to mRNA; 1538 BP.
XX AAV69886;
XX
XX 10-FEB-1999 (first entry)
XX
XX Nucleic acid encoding an OCIF-binding molecule (OBM).
XX
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
XX osteoclast; bone absorption factor; bone disorder; calcium metabolism;
XX ss.
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
XX CDS 125..1075
XX /*tag= a
XX
XX W09846644-A1.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
XX
XX 02-DEC-1997; 97JP-0332241.
XX 15-APR-1997; 97JP-0097808.
XX 09-JUN-1997; 97JP-0151434.
XX 12-AUG-1997; 97JP-0217897.
XX 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
XX Washida N, Yamaguchi K, Yano K, Yasuda H;
XX WPI: 1998-594563/50.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
XX for, e.g. treatment and investigation of disorders of bone and
XX calcium metabolism
XX
XX Claim 9; Pages 108-109; 151pp: Japanese.
XX
XX The present sequence encodes an osteoclastogenesis inhibitory factor
XX (OCIF)-binding molecule (OBM). The protein promotes and supports the
XX separation and maturation of osteoclasts in the presence of bone
XX absorption factors such as calcitriol or parathyroid hormone (PTH).
XX OBM is isolated from stroma cells cultured in the presence of a bone
XX absorption factor by separation and solubilisation of membrane proteins
XX then affinity chromatography using OCIF. It exists in a full-sequence
XX form and a solubilised form (SOBM) which is a shorter chain. OBM may be
XX used for screening potential inhibitors and modifiers of its biological
XX activity, and screening for receptors to OBM which mediate its function.
XX These substances can then be used in the treatment of disorders of bone
XX function and calcium metabolism. The antibodies can be used for assay
XX components of drugs.
XX
XX Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other;

Query Match 82.7%; Score 1348.4; DB 19; Length 1538;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1349; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGGCGTCCACACAGAGGGTCCGGCGACCCCGGCGCTTGTGACCGGCTCCGGCGCGC 60
|||
DB 189 ccggcggtcccaacagagggctcgcgcacccgcgcgttcgcacgcgcgtccgcgcgcgc 248
|||
OY 61 CACCCGCCCTCCCGCTCATGTTCCGTCGCCCCCTCTGGGCGTGGAGTGGCCAGGTG 120
|||
DB 249 caccgcgcctccgcgcctcctcctcgtccgcgcctcgcgcgcgcgcgcgcgcgcgcgc 308
|||
OY 121 TCTGACGATGCTCTGTTCTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 180
|||
DB 309 tctgacgactcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgt 368
|||
OY 181 AAGACGACGACTGCTGTTTATAGAAATCTGAGACCTGATGAAAGCGAGATTGGAGG 240
|||
DB 369 aagacgacgactcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctc 428
|||
OY 241 ACTGACTCTGGAAGTGAAGACACACTACTGACTCTGCTGAGAGGATGAACAGCT 300
|||
DB 429 actgactctggaagtgaagacacactactgactctgctgagaggtgaacagctctgag 488
|||
OY 301 TTCAGGGGGCGGTGACAGAGAACTGCACACATTTGGGGCCACAGCGTCTTCAGAG 360
|||
DB 489 ttcagggggcggtgacagagaaactgcacacatttggggccacagcgcttctcagag 548
|||
OY 361 CTCGAGCTATGATGAAGGCTCATGTTGATGTGGCCGACGAGGAGAGCGCTGAGCC 420
|||
DB 549 ctcgagctatgatgaaggctcatgttgatgtggccgacgagagagcgctgagcc 608
|||
OY 421 AGCCATTGGCAACCTCACTCAATGCTGCCACATCCATCGGTTCCCATAAAGTCA 480
|||
DB 609 agccattggcaacctcactcaatgctgccacatcccatcggttcccataaagtca 668
|||
OY 481 CTCTGCTCTTGTGTACAGATGAGGCTGGGCGCAAGTCTCTACATACGTTAAGCA 540
|||
DB 669 ctctgctcttgtgtacagatgaggtggcgcaagtctctacatacgtttaagca 728
|||
OY 541 ACGGAAACTAAGGGTTAACCAGATGGCTTCTATTACTGTACGCCAATTTGCTTTC 600
|||
DB 729 acggaaactaagggttaaccagatggcttctattactgtacgccaatTTGCTTTC 788
|||
OY 601 GGCATTCATGAACATCGGGAAGCTACTACAGACTTCTTACAGCTGATGTGATGTCG 660
|||
DB 789 ggcattcatgaacatcgggaagctactacagacttcttacagctgattgtgattcgc 848
|||
OY 661 TTAAGACGACGATCAAAATCCCAAGTTCATTAACCTGATGAAGAGGAGCAGCAAAA 720
|||
DB 849 ttaagacgacgatcaaaatcccaagtTCATTAACCTGATGAAGAGGAGCAGCAAAA 908
|||
OY 721 ACTGGTGGGCAATTCTGAATTCACCTTTATTCCATMAATGTTGGGGATTTTTCAGC 780
|||
DB 909 actggTGGGCAATTCTGAATTCACCTTTATTCCATMAATGTTGGGGATTTTTCAGC 968
|||
OY 781 TCCGAGTGTGGAAGAAATTAAGCATTTAGGTGCCAACCTTCCCTGCTGATCCGATC 840
|||
DB 969 tccgagTGTGGAAGAAATTAAGCATTTAGGTGCCAACCTTCCCTGCTGATCCGATC 1028
|||
OY 841 AAGATGCGAGCTACTTGGGGCTTCAAGTTCAGAGCATGAGTGAATTCATTTGCTG 900
|||
DB 1029 aagatgCGAGCTACTTGGGGCTTCAAGTTCAGAGCATGAGTGAATTCATTTGCTG 1088
|||
OY 901 GAACATTAGCATGGAGTCTCTAGATGTTTGAACCTTTTAAAAAATGATGATGCTAT 960
|||
DB 1089 gaacattAGCATGGAGTCTCTAGATGTTTGAACCTTTTAAAAAATGATGATGCTAT 1148
|||
OY 961 ACATGTGTAGACTACATTAAGAGCATGGCCAGGCTGATGAACATCAGCGCTCTTC 1020
|||
DB 1149 acatgtGTAGACTACATTAAGAGCATGGCCAGGCTGATGAACATCAGCGCTCTTC 1208
|||

Db	1118	atatacttcgtcgtacgatcttctgattccaaatatttaaaaatgcaccagttcgacata	1177
Oy	1485	TTTTAATGTTTTTAANTACAGATGTATTWTTAACTGGTGCACTTGTGAATTCCTGAAGT	1544
Db	1178	tctaagcttctaabaatgcagaatgaattacttaactggtgcacttg-aattccccgaagt	1236
Oy	1545	ACTCGTAGCTAAGGGGGCAGAATDAGCTGTTCTGGTGACCACACATGATGTTATTTCTTAT	1604
Db	1237	actcgtacctaaaggagcaaacacgttctctgtagccaacatgatttatcttcttat	1296
Oy	1605	TCTTTTAACTTAATAAGACTTTCAG	1630
Db	1297	tcctttaacttaacatagagctcttcag	1322
Result	12		
AA299964	ID	AA299964 standard: DNA; 2271 BP.	
XX	AC	AA299964;	
XX	DT	25-JUL-2000 (first entry)	
XX	DE	DNA encoding a human osteoprotegerin ligand (OPGL).	
XX	KM	Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;	
XX	KV	tumour necrosis factor receptor; type II transmembrane protein;	
XX	KW	osteoclast differentiation; CSF-1; osteoclast activator;	
XX	KW	immune response; osteoporosis; bone resorption; ss.	
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	FT	185..1138	
FT	CD5	/tag= a	
FT	FT	/product= "osteoprotegerin ligand"	
XX	XX	WO200015807-A1.	
XX	PD	23-MAR-2000.	
XX	PF	13-SEP-1999; 99WO-DK00481.	
PR	PR	15-SEP-1998; 98DK-0001164.	
BR	BR	02-OCT-1998; 98US-0102896.	
XX	PA	(MEBI-) M & E BIOTECH AS.	
PI	PI	Halkier T, Heanling J;	
XX	DR	WPI: 2000-271444/23.	
XX	DR	P-PDB: AAY84417.	
XX	XX	In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used	
XX	XX	to treat, prevent and ameliorate osteoporosis -	
PS	PS	Disclosure: Page 75-77; 110pp; English.	
CC	CC	The present sequence encodes a human osteoprotegerin ligand (OPGL).	
CC	CC	Osteoprotegerin is a secreted member of the tumour necrosis factor	
CC	CC	receptor family, which blocks osteoclastogenesis in a dose dependent	
CC	CC	manner. The OPGL protein is synthesised as a type II transmembrane	
CC	CC	protein. The murine and human OPGL polypeptides are 87% homologous. OPGL	
CC	CC	is a potent osteoclast differentiation factor when combined with CSF-1.	
CC	CC	It is not capable of inducing osteoclast differentiation in the absence	
CC	CC	of CSF-1. OPGL is also an activator of mature osteoclasts. The	
CC	CC	specification describes a method for the in vivo down-regulation of	
CC	CC	OPGL activity in an animal. The method comprises using at least one OPGL	
CC	CC	polypeptide or subsequence, and/or at least one OPGL analogue to induce	
CC	CC	an immune response in the animal. The method and OPGL polypeptide are	
CC	CC	useful for treating, preventing and ameliorating osteoporosis or other	
CC	CC	diseases or conditions characterised by excessive bone resorption.	

[illegible]

Query Match	54.3%;	Score 885.4;	DB 19;	Length 951;
Best Local Similarity	99.9%;	Pred. No. 2.8e-223;		
Matches 886;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	CCCCGCGCCACAGAGGGGTCGCTCACCCCGCGCTTCTGACGCGCTCCGGCGCGC	60
OY	65	ccccgcgtcccaacaagaaggttcgcgtgcacccgcgccttcctgcacccggtccggcgccg	124
Db	61	CACCCGCGGCTCCCGCTCCAGTTCCTGAGCCTCTGGAGCTGGGACTGGGCAAGTGG	120
OY	125	caaccgcgcctcccgctccatgctatgctctgcccctctgggctcgtggaactcggccagtgg	184
Db	121	TCGCGACCATCGCTCTGCTTCCTGACTTCGAGCGAGATGGATCTCTAACAGATATCAG	180
OY	185	tcgtcagcatctgcctgtcttcctgtaacttcgagcgcaagatggatcccaagaatctcag	244
Db	181	AAGACACACACTACTGCTTTTATAGATCCTGAGACTCCATGAAACGCAAGATTTGCAAG	240
OY	245	aagcagcagactcactgcttttatagaatcctcgtgactccatgaaacgcaggtgttcag	304
Db	241	ACTGCACTCTGAGAGTGAAGACACACTACTCTGACTCTGACAGAGATGAAACAAGCCT	300
OY	305	actgcaactctgagatgtaagaacacatacttactcttcgcagtagatgtaaacagacct	364
Db	301	TTTCAGGGGCGCGTCACAAAGAACTGCACACATTGCGGGGCACAGCGCTTCTTCAGAG	360
OY	365	ttcagggggccgtgcagaaggaactcgtaaacattgtgggccaacagcgctcttcaggg	424
Db	361	CTCCAGCTATGATGGAAGGCTCATGTGTGATGTGGCCAGCGAAGCAAGCTCGAAGCCC	420
OY	425	ctcagcatgatgtgaagagctcatalgtgttgatgtgcccagcgaggaagcctgcgaagccc	484
Db	421	AGCCATTTGGCACACCTCACCATCAATGCTGGCACACATCCCATGGGTTCCCATAAAGTCA	480
OY	485	aagcaatttgcacactccacccaatcgaatcgtccgcagcatcccatcgtgttcccataaagtca	544
Db	481	CTCTGTCTCTTTGGTACACAGATGAGGCGTGGGCCAAGATCTCTAACATGAGCTTAAACA	540
OY	545	ctctgtctcttgttaccagatctcgaagctcgggcacaagatccttaacatgactgtaagca	604
Db	541	ACGGAAACTTAAGGTTTACCAACATGGCTCTTATACGTACAGCCACAAATTGGCTTC	600
OY	605	acggaacaactaagggttaacacaagaatggtctctatcccgtaagcacaacattgtcttc	664
Db	601	GGCATCATGAACAATCGGGAGCGCTACCTACAGACTATCTTCAGCTGATGGTGAATCG	660
OY	665	ggtcatcatgaaacatcgggaagcgctacctacagactatcttcagctgagtgtatgtcg	724
Db	661	TTTAAACACGACATCAAAATCCCAAGTTCTCTAATCCTGATGAAGGAAGGACACGAAA	720
OY	725	tttaaaacacagatcatcaaaatcccaagttctctaaacctgataaaagagggagacgaaaa	784
Db	721	ACTGTCGGGGCAATCTGAAATTTCCACTTTTATCCATTAATATGTTGGGGGATTTTTCAGC	780
OY	785	actggttcgggcacatctgtaattccactttatccataaaatglttgggggatttttcaagc	844
Db	781	TCGCGAGCTGGTAAAGAAATTAGACTTCAGGTGTCCAAACCTTTCCTGCTGGATCCGATC	840
OY	845	tcgagctggtgtaagaataatgacatctcaggtgtccaaaccttcctgtcgtgatacggatc	904
Db	841	AAGATGCCAGCTACTTTGGGGCTTTCAAAGTTTCAGAGATATGACTGA 887	
OY	905	aagatgtcgagctactcttgggtcttcaaaagttcaggaataatgactgca 951	

```

RESULT 15
AAA39156
ID AAA39156 standard; DNA; 951 BP.
XX
AC AAA39156;
XX

```

DT	05-SEP-2000	(first entry)
XX		
DE	Mouse OBM nucleotide sequence	SEQ ID NO:9

AA Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF.
 KM OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH.
 KW parathyroid hormone; ds.

Mus sp.

PN JP2000102390-A.

PD 11-APR-2000.

PF 30-SEP-1998; 98JP-0292971.

PR 30-SEP-1998; 98JP-0292971.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

XX

DR P-PSDB; AAY91024

PT A DNA and preparation of a protein by using it

PS Example 1; Page 15; 18pp; Japanese.

AX The present invention describes a genomic DNA encoding a protein having
CC an activity of supporting or promoting differentiation and maturation of
CC osteoclasts. The genomic DNA encoding a protein has the following
CC properties: (a) combines specifically with osteoclastogenesis inhibitory
CC factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)
CC of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide
CC gel electrophoresis) under a nonreductive condition and the apparent mw
CC then crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)
CC has an activity of supporting or promoting differentiation and maturation
CC of osteoclast in the co-culture of mouse osteoblast-like stroma cell and
CC mouse spleen cell in the presence of a bone absorption promoting factor
CC such as active type vitamin D3 and parathyroid hormone (PTH). The protein
CC can be used as a drug and a research reagent. The present sequence
CC encodes a mouse OCIF binding molecule (OBM) from the present invention.

aa Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
SO

Query Match	54.3%	Score 885.4	DB 21	Length 951
Best Local Similarity	99.9%	Pred. No. 2.8e-223		
Matches 886: Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	CGGCGCTCCACAGAGGAGTCCGCTGCACCCCGCCTTCTGCACCGGCTCCGGGCGCG	60
Db	65	ccgagctcccaacagaggtccgcgtgcaccccgccctctgcacccggtcccgccgcg	124
QY	61	CACCGCGCCCTCCCGGCTGCATGTTCCCGGGCCCTCGGGGCTAGGACTGGCGCAGGTGG	120
Db	125	caaccgcgcctcccgctccacatgcttcctgcgccccttcgggcttcggagactcggccagttcg	184
QY	121	TCMGACGACTGCCTCTGTGTTCCGTACTTTTCAGCGCAGATGGATCTTCACAGATAATCAG	180
Db	185	tctgcgaagtcgcctcgtctcgtctcgtactccttcgagcgcagatggaatccctacaagaatatcag	244
QY	181	AAGACGACACTACTGCTTTTATTAGAAATCCTGAGACTCCATGAAGACGAGATTTGCAGC	240
Db	245	aagacgcgcctcactcgtctttatagatcctcgagatccatgaaacgcagtttgag	304
QY	241	ACTCGACTCTGAGAGAGTAGAGACACACTTACTGACTCTGAGAGAGATGAACCAACCT	300
Db	305	actcgactctggagaggtgagacacacactcgtactcctgacgagaggaatgaacaagcct	364
QY	301	TTTAGGGGCGCGTGCAGAGGAACCTGGCAACCATTTGTGGGCGCACAGCGCTTCACAGAG	360
Db	365	ttcaaggaggcctctgcagaaagaaactgcacaacatctgtgggcccacagcgtctctcagag	424

Oy	361	CTCAAGACTTGAATGGAAGGCTTCATGTTGGATGTGCGCCACGAGGCGAAGACTTGAGGCC	420
Db	425	ctccagcctctgctggaaggctctcaatggtctggaatgtggtcccgagcgagcaagcttgagcccc	484
Oy	421	AGCCATTTTGACACCACTGCACATCATGCTGGCAGACATCCCATCGGGGTTCCTCAATGAATCA	480
Db	485	agccattctgcacacctcctacatcaaatgctgtccagcaatcccatctgggtcttcccaataagctca	544
Oy	481	CTCTTCCTCTTGGTACACACATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGA	540
Db	545	ctctgtccctcttggtaccacgactcggaagcttggtgcagaagatctctcaacatgaagcttaagca	604
Oy	541	ACGGAAMAATAAGGTTTAAACAATGGCTCTTTACCTGTACGGCAACATTTGGTTTC	600
Db	605	acggaanaactaagggttaacacagaatggtctctcatcttaccgtgaagccaaatctgtcttc	664
Oy	601	GGCATTCATGAANAACATCGGGAAGGCTACCTACAGACTATCTTCAGCTGATGTTATGTGC	660
Db	665	ggcatcatcgaaacatcggaagctgtacctacagactcttcttcagctggaatggttgaatctcg	724
Oy	661	TTTAAACCAAGCATCAAAATCCCAAGTTCTCTATAACGATGAAGAAGAGAGACCAAAA	720
Db	725	ttaaaaccagcatcctcaaaatcccaagttctctataacctgatgaagaaggaaggagcaagaaaa	784
Oy	721	ACTGGTCGGGCAATTTCGAAATTCCACTTTTATTCATTAATGTTGGGGCATTTTTCACG	780
Db	785	actggttcggggaattctcgaaatcccaatcttattccataaattgttggggaatttcttaagc	844
Oy	781	TCCGAGCTGCTGAAGAAATTAGCATTCAGGTGTCAACACCTTCCCTGCTGGATTCGGGATC	840
Db	845	tccgagcttggtgaaagaaattagcatctcaagtgtgtccaaacctctccgtcgtgataccggtatc	904
Oy	841	AAGATCGGAGGTAATCTTGGGGGCTTCAAAAGTTAGACATAGACTGA	887
Db	905	aagatcgagcttaactcttggtggcttctccaagttctcaagataactgaactga 951	

Search completed: July 8, 2002, 21:43:41
Job time: 6075 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 19:52:41 ; Search time 96.15 Seconds
(without alignments)
4164.146 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630
Sequence: 1 CCGCGCTCCACACGAGGCT.....TAAGTTAATAGAGTCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: /cgn2_6/ptcodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptcodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptcodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptcodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptcodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptcodata/2/lna/backfilese1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1630	100.0	1630	3 US-08-996-139-10	Sequence 10, App1
2	1630	100.0	1630	4 US-08-995-659-10	Sequence 10, App1
3	1630	100.0	1630	4 US-09-215-649A-10	Sequence 10, App1
4	1628.4	99.9	2295	2 US-08-842-842-6	Sequence 6, App1
5	1628.4	99.9	2295	4 US-09-052-521C-1	Sequence 1, App1
6	1615.8	99.1	2191	4 US-08-989-362-1	Sequence 3, App1
7	939.6	57.6	2271	4 US-09-052-521C-3	Sequence 1, App1
8	615	37.7	954	3 US-08-996-139-12	Sequence 12, App1
9	615	37.7	954	4 US-08-995-659-12	Sequence 12, App1
10	615	37.7	954	4 US-09-215-649A-12	Sequence 12, App1
11	58.4	3.6	759	4 US-09-320-424-10	Sequence 10, App1
12	58.4	3.6	768	4 US-09-320-424-12	Sequence 12, App1
13	58.4	3.6	1042	3 US-08-584-031-2	Sequence 10, App1
14	58.4	3.6	1042	3 US-08-780-496-2	Sequence 2, App1
15	58.4	3.6	1521	1 US-08-670-354-3	Sequence 3, App1
16	58.4	3.6	1521	4 US-09-320-424-3	Sequence 3, App1
17	58.4	3.6	1521	5 PCT-US96-10895-3	Sequence 3, App1
18	58.4	3.6	1751	1 US-08-670-354-1	Sequence 1, App1
19	58.4	3.6	1751	4 US-09-320-424-1	Sequence 1, App1
20	58.4	3.6	1751	5 PCT-US96-10895-1	Sequence 1, App1
21	58.4	3.6	1769	4 US-09-333-593A-5	Sequence 5, App1
22	58.4	3.6	1769	4 US-09-505-250-1	Sequence 5, App1
23	58.4	3.6	1769	4 US-09-320-424-5	Sequence 5, App1
24	58.4	3.6	1769	4 US-08-670-354-5	Sequence 5, App1
25	58.4	3.6	1769	4 US-09-320-424-5	Sequence 5, App1
26	58.4	3.6	1769	4 US-09-320-424-5	Sequence 5, App1
27	58.4	3.6	1769	4 US-08-751-359-21	Sequence 21, App1

C	28	45.2	2.8	688	4 US-08-998-416-972	Sequence 972, App
	29	45	2.8	662	4 US-08-998-416-185	Sequence 185, App
	30	45	2.8	665	4 US-08-998-416-937	Sequence 937, App
	31	45	2.8	701	4 US-08-998-416-701	Sequence 701, App
	32	45	2.8	724	4 US-08-998-416-683	Sequence 683, App
	33	45	2.8	732	4 US-08-998-416-1036	Sequence 1036, App
	34	45	2.8	767	4 US-08-998-416-472	Sequence 472, App
	35	45	2.8	827	4 US-08-998-416-535	Sequence 535, App
	36	45	2.8	828	4 US-08-998-416-538	Sequence 538, App
	37	45	2.8	834	4 US-08-998-416-305	Sequence 305, App
	38	44.8	2.7	711	4 US-08-998-416-786	Sequence 786, App
C	39	44.2	2.7	6132	4 US-08-973-462-1	Sequence 1, App1
C	40	43.4	2.7	6243	2 US-09-056-075-1	Sequence 1, App1
C	41	43.2	2.7	19124	2 US-08-487-8268-13	Sequence 13, App1
	42	42.2	2.6	782	4 US-08-998-416-224	Sequence 224, App
	43	41.6	2.6	6124	4 US-08-213-4198-3	Sequence 3, App1
	44	41.4	2.5	1826	4 US-09-286-691-11	Sequence 11, App1
C	45	41.4	2.5	1826	4 US-09-687-147-11	Sequence 11, App1

ALIGNMENTS

RESULT 1
US-08-996-139-10
; Sequence 10, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1630 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
IMMEDIATE SOURCE:
LIBRARY:
CLONE: RANKL
FEATURE:
NAME/KEY: CDS
LOCATION: 3..884
US-08-995-659-10

Query Match 100.0%; Score 1630; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCGGCGTCCACAGAGAGTCCGCTGACACCCGCGCTTCTGCACCGAGTCCGGCGCGC 60
1 CCGGCGTCCACAGAGAGTCCGCTGACACCCGCGCTTCTGCACCGAGTCCGGCGCGC 60
61 CACCGCGCGCTCCCGCTCCATGTTCTCTGGCCCTCTGGGGCTTGGAGTGGGCCAGGTG 120
61 CACCGCGCGCTCCCGCTCCATGTTCTCTGGCCCTCTGGGGCTTGGAGTGGGCCAGGTG 120
61 CACCGCGCGCTCCCGCTCCATGTTCTCTGGCCCTCTGGGGCTTGGAGTGGGCCAGGTG 120
121 TCTGCAGATCGCTCTGCTTCTCTGACTTTGAGAGCGAGATGATCTCAACAGATATACAG 180
121 TCTGCAGATCGCTCTGCTTCTCTGACTTTGAGAGCGAGATGATCTCAACAGATATACAG 180
121 TCTGCAGATCGCTCTGCTTCTCTGACTTTGAGAGCGAGATGATCTCAACAGATATACAG 180
181 AAGACAGACTGCTGCTTTATAGAACTGAGACTGCATGAAAGAGAGATTTGAGG 240
181 AAGACAGACTGCTGCTTTATAGAACTGAGACTGCATGAAAGAGAGATTTGAGG 240
181 AAGACAGACTGCTGCTTTATAGAACTGAGACTGCATGAAAGAGAGATTTGAGG 240
241 ACTGACTCTGGAGAGTGAAGACACACTACCTGACTCTCGAGAGGATGAACAAAGCCT 300
241 ACTGACTCTGGAGAGTGAAGACACACTACCTGACTCTCGAGAGGATGAACAAAGCCT 300
301 TTCAGGGGGCGGTGCAAGAACTGCAACACTTGTGGGCCACACGCTTCTCAGAG 360

|||||
Db 301 TTCAGGGGGCGGTGCAAGAACTGCAACACTTGTGGGCCACACGCTTCTCAGAG 360
Qy 361 CTCGAGCTATGATGGAAGGCTCATGTTGATGTGGCCACGAGGAGCCTGAGGCC 420
Db 361 CTCGAGCTATGATGGAAGGCTCATGTTGATGTGGCCACGAGGAGCCTGAGGCC 420
Qy 421 AGCATTGGCACACCTGACCATGCAATGCTGACACATCCCATGGGTTCCTTAATCA 480
Db 421 AGCATTGGCACACCTGACCATGCAATGCTGACACATCCCATGGGTTCCTTAATCA 480
Qy 481 CTCTGCTCTTGGTACACGATGAGGCTGGGCCAAGATCTTAACATGACGTTAAGCA 540
Db 481 CTCTGCTCTTGGTACACGATGAGGCTGGGCCAAGATCTTAACATGACGTTAAGCA 540
Qy 541 ACGGAAACTTAAGGTTTACCAGATGCTTATTAACCTGTACGCCACATTTGCTTC 600
Db 541 ACGGAAACTTAAGGTTTACCAGATGCTTATTAACCTGTACGCCACATTTGCTTC 600
Qy 601 GGCATCATGAAACATCGGGAAGCTACCTACAGACTATCTTACGCTGATGGTATGTCG 660
Db 601 GGCATCATGAAACATCGGGAAGCTACCTACAGACTATCTTACGCTGATGGTATGTCG 660
Qy 661 TTAACACGATCAAAATCCCAAGTTCTCATTAACCTGATGAAAGAGGAGCAGAAAA 720
Db 661 TTAACACGATCAAAATCCCAAGTTCTCATTAACCTGATGAAAGAGGAGCAGAAAA 720
Qy 721 ACTGCTGGGCAATCTGAAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGC 780
Db 721 ACTGCTGGGCAATCTGAAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGC 780
Qy 781 TCCGAGCTGTGAAGAAATTAGCTTACGATGTCACACCCCTCCCTGATGCCGATC 840
Db 781 TCCGAGCTGTGAAGAAATTAGCTTACGATGTCACACCCCTCCCTGATGCCGATC 840
Qy 841 AAGATCGACGTAATTTGGGGCTTCAAGTTCAAGATCAGACATAGACTGATTTGCTG 900
Db 841 AAGATCGACGTAATTTGGGGCTTCAAGTTCAAGATCAGACATAGACTGATTTGCTG 900
Qy 901 GAACATTAAGATGATGCTCTAGATGTTTGGAAATCTTAAAAAATGATGATGCTAT 960
Db 901 GAACATTAAGATGATGCTCTAGATGTTTGGAAATCTTAAAAAATGATGATGCTAT 960
Qy 961 ACATGTGTAAGACTACTTAAGACATGAGCCACGCTGATGAACACTACAGCCCTCTCTC 1020
Db 961 ACATGTGTAAGACTACTTAAGACATGAGCCACGCTGATGAACACTACAGCCCTCTCTC 1020
Qy 1021 TTGAGCTGTACAGTGTGTATATGTAAGTCCATAGTGTATGATTTCAATGCTGAT 1080
Db 1021 TTGAGCTGTACAGTGTGTATATGTAAGTCCATAGTGTATGATTTCAATGCTGAT 1080
Qy 1081 TACACAAGGTTTACAAATTTGTAATGATTTCCCTAGAAATTTGAACCAAGATTTGGAAGAGT 1140
Db 1081 TACACAAGGTTTACAAATTTGTAATGATTTCCCTAGAAATTTGAACCAAGATTTGGAAGAGT 1140
Qy 1141 ATTCCGATGCTTATGAAAACTTACAGTGAAGTATGGAAGGGGGTACAGTCTTGAGT 1200
Db 1141 ATTCCGATGCTTATGAAAACTTACAGTGAAGTATGGAAGGGGGTACAGTCTTGAGT 1200
Qy 1201 CTAAACCCCTGACATGTCGACAGAGAACTGAAATTAAGAGATGCCATGTCATTGCA 1260
Db 1201 CTAAACCCCTGACATGTCGACAGAGAACTGAAATTAAGAGATGCCATGTCATTGCA 1260
Qy 1261 AAGAAATGATAGTGAAGGTTAAGTCTTTGGAATGTTTACATGTCGCTGGAGACTGC 1320
Db 1261 AAGAAATGATAGTGAAGGTTAAGTCTTTGGAATGTTTACATGTCGCTGGAGACTGC 1320
Qy 1321 AAATTAAGTCTTTTCTTAATGAGAGGAAATAATATATATTTTATATATGCTTA 1380
Db 1321 AAATTAAGTCTTTTCTTAATGAGAGGAAATAATATATATTTTATATATGCTTA 1380
Qy 1381 AAGTATATTTCAAGTGTAAATGTTTCTGTGCAAGTTTTGAATTAATTTTGTCTAT 1440
Db 1381 AAGTATATTTCAAGTGTAAATGTTTCTGTGCAAGTTTTGAATTAATTTTGTCTAT 1440

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	Best Local Similarity	Score 1630;	DB 4;	Length 1630;
Matches 1630;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	CCGCGCTCCACAGAGGGTCCGCTGACACCCCGGCGCTTCTGCAACCGGCTCCGGGCGCCG	100.0%;		
1	CCGGGTCCCAACAGAGGGTCCGCTGACACCCCGGCGCTTCTGCAACCGGCTCCGGGCGCCG	100.0%;		
61	CACCGCGCGCTCCCGCTCCACATGTTCCCGGCGCTCTGAGGCTGGGACTGGGCGCAAGTGG			
61	CACCGCGCGCTCCCGCTCCACATGTTCCCGGCGCTCTGAGGCTGGGACTGGGCGCAAGTGG			
121	TCGCGAGCATGCGTCTGTCTGTTCTGACATTTCGAGCGCAGATGGATCTTAACAGAAATATAG			
121	TCGCGAGCATGCGTCTGTCTGTTCTGACATTTCGAGCGCAGATGGATCTTAACAGAAATATAG			
181	AAGACAGACATCAGCTTTTATAGAAATCCTGAGACTCCATGAAACCCAGATTTCAGG			
181	AAGACAGACATCAGCTTTTATAGAAATCCTGAGACTCCATGAAACCCAGATTTCAGG			
241	ACTGCACTGTGAGAGTAGAAGACACACTACTGACTCTCTGACAGAGATGAACAAGCTT			
241	ACTGCACTGTGAGAGTAGAAGACACACTACTGACTCTCTGACAGAGATGAACAAGCTT			
301	TTGACGGGGCGCGTGAGAAGAACTGCAAAACATTGTGGGGCACAGGCTTCTCAGAG			
301	TTGACGGGGCGCGTGAGAAGAACTGCAAAACATTGTGGGGCACAGGCTTCTCAGAG			
361	CTCCAGTATGATGGAAGGGCTCATGGTTGATGTGGCCAGCGAGGCAAGCCTGAGGCC			
361	CTCCAGTATGATGGAAGGGCTCATGGTTGATGTGGCCAGCGAGGCAAGCCTGAGGCC			
421	AGCCATTGTCACACCTCACATCATGCTGCGCAGATCCCATCGGGTCCCTAAAGTCA			
421	AGCCATTGTCACACCTCACATCATGCTGCGCAGATCCCATCGGGTCCCTAAAGTCA			
481	CGCTGCTCTGTTGATGACAGCATGATCGAGGCTGGGCCAAGATCTCTAAATGACGTTAAGCA			
481	CGCTGCTCTGTTGATGACAGCATGATCGAGGCTGGGCCAAGATCTCTAAATGACGTTAAGCA			
541	ACGGAACCTAAGGGTTAAACCAAGATGCTTATTAACCTGTAACGCAACATTTGCTTTC			
541	ACGGAACCTAAGGGTTAAACCAAGATGCTTATTAACCTGTAACGCAACATTTGCTTTC			
601	GGCATCATGAAACATCGGGGAAGCGTACACACATATTTAGCTGATGGTGTATGTG			
601	GGCATCATGAAACATCGGGGAAGCGTACACACATATTTAGCTGATGGTGTATGTG			
661	TTTAAACCCAGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGGACACGAAAA			
661	TTTAAACCCAGATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGAGGACACGAAAA			
721	ACTGGTCGGGCAATTCGAAATTCACATTTTATTCATTAATGTGGGGATTTTTCACAC			
721	ACTGGTCGGGCAATTCGAAATTCACATTTTATTCATTAATGTGGGGATTTTTCACAC			
781	TCGCGACTGTGAAGAAATTAAGATCAAGGTGCAACCCCTCCGCTGATTCGGATC			
781	TCGCGACTGTGAAGAAATTAAGATCAAGGTGCAACCCCTCCGCTGATTCGGATC			
841	AAGATCGACGATCTTTGGGGCTTTCAAGTTTCAGACATTAACATGACTATTTCTG			
841	AAGATCGACGATCTTTGGGGCTTTCAAGTTTCAGACATTAACATGACTATTTCTG			
901	GAAATTAACATGATGCTGATGTTGAAATCTTAAATAATGATGATGCTAT			

Db 901 GAACATTAGCATGATGCTAGATGTTGGAACTTCTTAAAAAATGATGATGCTAT 960
Qy 961 ACATGTGTAAAGACTACTAAGAGACATGGCCACGGTGTATGAACCTACAGCCCTCTC 1020
Db 961 ACATGTGTAAAGACTACTAAGAGACATGGCCACGGTGTATGAACCTACAGCCCTCTC 1020
Qy 1021 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGGTGATGATTCATGTGTAT 1080
Db 1021 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGGTGATGATTCATGTGTAT 1080
Qy 1081 TACACAACGGTTTTTACAAATTTTGAATGATTTCTTGAATGAACCAAGATGGGAGAGT 1140
Db 1081 TACACAACGGTTTTTACAAATTTTGAATGATTTCTTGAATGAACCAAGATGGGAGAGT 1140
Qy 1141 ATTCCGATGCTTATGAAAAAATTACACGTAGCTATGGAAGGGGTACAGTCTGGGT 1200
Db 1141 ATTCCGATGCTTATGAAAAAATTACACGTAGCTATGGAAGGGGTACAGTCTGGGT 1200
Qy 1201 CTAAACCCCTGGACATGTGACACCTGAGAACCTTGAATTAAGAGATGCAATGTCAT 1260
Db 1201 CTAAACCCCTGGACATGTGACACCTGAGAACCTTGAATTAAGAGATGCAATGTCAT 1260
Qy 1261 AAGAAATGATAGTGTGAAGGTTAAGTCTTTGAATGTTTACATGGCGTGGAGACTGC 1320
Db 1261 AAGAAATGATAGTGTGAAGGTTAAGTCTTTGAATGTTTACATGGCGTGGAGACTGC 1320
Qy 1321 AAATAGCTCTTTTCTTATGAGAGAGAAAAATATATGATTTTATATATGCTTA 1380
Db 1321 AAATAGCTCTTTTCTTATGAGAGAGAAAAATATATGATTTTATATATGCTTA 1380
Qy 1381 AAGTTATATTCAGGATGATATGTTTCTGTGCAAAAGTTTGAATTAATTTGTCAT 1440
Db 1381 AAGTTATATTCAGGATGATATGTTTCTGTGCAAAAGTTTGAATTAATTTGTCAT 1440
Qy 1441 AGTATTTGATTTAAATATTTTAAATGCTCAGTGTGACATATTTATTTTAAAG 1500
Db 1441 AGTATTTGATTTAAATATTTTAAATGCTCAGTGTGACATATTTATTTTAAAG 1500
Qy 1501 TACAGATGATTTAACTGTGACCTTTGTAATTCCTTGAAGTACTGCTAAGGG 1560
Db 1501 TACAGATGATTTAACTGTGACCTTTGTAATTCCTTGAAGTACTGCTAAGGG 1560
Qy 1561 GCAGATGATTTTCTGTGAGACACATGATTTTCTTTATTTTAACTTAATTA 1620
Db 1561 GCAGATGATTTTCTGTGAGACACATGATTTTCTTTATTTCTTTTAACTTAATTA 1620
Qy 1621 GAGCTTTACAG 1630
Db 1621 GAGCTTTACAG 1630

RESULT 4
US-08-842-842-6
Sequence 6, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842

FILED DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 158..1105
US-08-842-842-6

Query Match 99.9% Score 1628.4; DB 2; Length 2295;
Best Local Similarity 99.9% Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGCTCCACACAGAGGTCGGTGCACCCCGGCTTCTGACCGGCTCCGGCGGC 60
Db 222 CCGGGCTCCACACAGAGGTCGGTGCACCCCGGCTTCTGACCGGCTCCGGCGGC 281
Qy 61 CACCGCGGCTCCCGCTCCATGTTTCTGSCCTCTGCGGCTGGAGTGGCCAGGTG 120
Db 282 CACCGCGGCTCCCGCTCCATGTTTCTGSCCTCTGCGGCTGGAGTGGCCAGGTG 341
Qy 121 TCTGAGCATGCTCTGTTCTGTTACTTTGAGGGGCAAGTGGATCTTACAGAAATATCAG 180
Db 342 TCTGAGCATGCTCTGTTCTGTTACTTTGAGGGGCAAGTGGATCTTACAGAAATATCAG 401
Qy 181 AAGACGACCTCCTCTTTTATAGAAATCTGAGACTCCATGAAGAACGAGATTGGCAGG 240
Db 402 AAGACGACCTCCTCTTTTATAGAAATCTGAGACTCCATGAAGAACGAGATTGGCAGG 461
Qy 241 ACTGAGCTCTGAGAGTGAAGACACTACTGACTCTCTGAGAGAGATGAACAAAGCCT 300
Db 462 ACTGAGCTCTGAGAGTGAAGACACTACTGACTCTCTGAGAGAGATGAACAAAGCCT 521
Qy 301 TTGAGGGGGCGGTCCAGAGAACTGCACACATTTGTGGGGCCACAGCGCTTCTCAGGAG 360
Db 522 TTGAGGGGGCGGTCCAGAGAACTGCACACATTTGTGGGGCCACAGCGCTTCTCAGGAG 381
Qy 361 CTCAGCTATGATGGAAGGCTCATGTTGATGTGGCCACAGGAGCAAGCCCTGAGGCC 420
Db 582 CTCAGCTATGATGGAAGGCTCATGTTGATGTGGCCACAGGAGCAAGCCCTGAGGCC 641
Qy 421 AGCCATTTGACACCTCACCATCAATGCTGCGAGCATCCCATGGGTTCCCATAAAGTCA 480
Db 642 AGCCATTTGACACCTCACCATCAATGCTGCGAGCATCCCATGGGTTCCCATAAAGTCA 701
Qy 481 CTCTGCTCTTGGTATCACAGATGAGGCTGGGCCAAGATCTCTAATGATGAGCTTAAGA 540
Db 702 CTCTGCTCTTGGTATCACAGATGAGGCTGGGCCAAGATCTCTAATGATGAGCTTAAGA 761
Qy 541 ACGGAATCTAAGGTTAAACCAAGATGCTTATTAACCTGTAAGCCCAATTTGCTTTC 600
Db 762 ACGGAATCTAAGGTTAAACCAAGATGCTTATTAACCTGTAAGCCCAATTTGCTTTC 821
Qy 601 GGCATCATGAACATGGGAGGCTACCTATGCTTACGCTGATGAGTGTATGTCG 660
Db 822 GGCATCATGAACATGGGAGGCTACCTATGCTTACGCTGATGAGTGTATGTCG 881
Qy 661 TTAAACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGACAGCAAAA 720
Db 882 TTAAACGACATCAAAATCCCAAGTTCTCATTAACCTGATGAAGAGGAGACAGCAAAA 941
Qy 721 ACTGTCGGGCAATTCGATTCACATTTTATTCATTAATGTTGGGGATTTTTCACAG 780
Db 942 ACTGTCGGGCAATTCGATTCACATTTTATTCATTAATGTTGGGGATTTTTCACAG 1001

```
OY 781 TCCGAGCTGTGAAGAAATAGATTCAGTGTCCAAACCCCTCCCTGCTGATCCGATC 840
|||||
Db 1002 TCCGAGCTGTGAAGAAATAGATTCAGTGTCCAAACCCCTCCCTGCTGATCCGATC 1061
|||||
OY 841 AAGATGCAGCTACTTTGGGGCTTTCAAAGTTCCAGACATATGACTGAGACATTTGGTG 900
|||||
Db 1062 AAGATGCAGCTACTTTGGGGCTTTCAAAGTTCCAGACATATGACTGAGACATTTGGTG 1121
|||||
OY 901 GAACATTTAGCATGATGCTCTAGATGTTTGAAGAACTTTAAAAAATGATGATGTCAT 960
|||||
Db 1122 GAACATTTAGCATGATGCTCTAGATGTTTGAAGAACTTTAAAAAATGATGATGTCAT 1181
|||||
OY 961 ACATGTGTAAAGACTACTAAGACATGCCCCAGGTGTATGAACTCACAGCCCTCTCTC 1020
|||||
Db 1182 ACATGTGTAAAGACTACTAAGACATGCCCCAGGTGTATGAACTCACAGCCCTCTCTC 1241
|||||
OY 1021 TTGAGCCCTGTACAGTTGTGTATGTAAAGTCCATAGGTGATGTATGATTCATGATGAT 1080
|||||
Db 1242 TTGAGCCCTGTACAGTTGTGTATGTAAAGTCCATAGGTGATGTATGATTCATGATGAT 1301
|||||
OY 1081 TACACAACGGTTTACAAATTTTGTATGATTTCTTGAATTTGAACCAAGATTGGAGAGGT 1140
|||||
Db 1302 TACACAACGGTTTACAAATTTTGTATGATTTCTTGAATTTGAACCAAGATTGGAGAGGT 1361
|||||
OY 1141 ATTCCGATCTTATGAAAAAATTACACCTGACGTATGGAAGGGGGTCCACAGTCTGGGT 1200
|||||
Db 1362 ATTCCGATCTTATGAAAAAATTACACCTGACGTATGGAAGGGGGTCCACAGTCTGGGT 1421
|||||
OY 1201 CTAAACCCCTGGACATGTCGACCTGAGAACCTTGAATTTAAGAGATGCCATGTCAATTGCA 1260
|||||
Db 1422 CTAAACCCCTGGACATGTCGACCTGAGAACCTTGAATTTAAGAGATGCCATGTCAATTGCA 1481
|||||
OY 1261 AAGAAATGATAGTGTGAGGGTTAAGTCTTTTGAATTTGTACATTGGCCCTGGACCTGC 1320
|||||
Db 1482 AAGAAATGATAGTGTGAGGGTTAAGTCTTTTGAATTTGTACATTGGCCCTGGACCTGC 1541
|||||
OY 1321 AATTAAGTCTTTTCTTAATGAGAGAGAAAAATATATGATTTTATATATGTCCTA 1380
|||||
Db 1542 AATTAAGTCTTTTCTTAATGAGAGAGAAAAATATATGATTTTATATATGTCCTA 1601
|||||
OY 1381 AAGTTATTTTCAAGTGTATATGTTTCTGTGCAAGTTTGTAAATTTATTTTGTCTAT 1440
|||||
Db 1602 AAGTTATTTTCAAGTGTATATGTTTCTGTGCAAGTTTGTAAATTTATTTTGTCTAT 1661
|||||
OY 1441 AGATTTTGAATTCAAATATTTAAAAATGCTCATCTGTGACATATTAATGTTTAAAG 1500
|||||
Db 1662 AGATTTTGAATTCAAATATTTAAAAATGCTCATCTGTGACATATTAATGTTTAAAG 1721
|||||
OY 1501 TACAGATGTTTAACTGCTGACACTTTGTAATTCCTCTGAAGGTACTGTAAGCTAAGGG 1560
|||||
Db 1722 TACAGATGTTTAACTGCTGACACTTTGTAATTCCTCTGAAGGTACTGTAAGCTAAGGG 1781
|||||
OY 1561 GCAGAAATACGTGTTTGTGTCGACACACATGATGTTTATTTCTTTTATCTTTTAACTAATA 1620
|||||
Db 1782 GCAGAAATACGTGTTTGTGTCGACACACATGATGTTTATTTCTTTTAACTAATA 1841
|||||
OY 1621 GAGCTTTCAG 1630
|||||
Db 1842 GAGCTTTCAG 1851
|||||
```

RESULT 5
US-09-052-521C-1
; Sequence 1, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855

```
; PRIOR FILING DATE: 1997-06-23  
; PRIOR APPLICATION NUMBER: 08/842,842  
; PRIOR FILING DATE: 1997-04-16  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2295  
; TYPE: DNA  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (158)..(1105)  
US-09-052-521C-1
```

Query Match 99.98; Score 1628.4; DB 4; Length 2295;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 CCGGCGTCCACAGAGAGGTCCGCTGACCCCGGCTTGTGACCGGCTCCGGCCGC 60
|||||
Db 222 ccggcggtccacaagaggggtccgctgaccccggtcttgacccggtccggccgc 281
|||||
OY 61 CACCCGCCGCTCCCGCTCCATGTTCTCGGCCCTCCTGSGACTGGCCAGGTG 120
|||||
Db 282 caccgcgcctcccgctcccaagctcgtccgctcccgagcgcgagcgtggccaggtg 341
|||||
OY 121 TCTGAGCATGCTCTGTTCTCTGTTCTGACTTTGAGCGCAGATGATCTTACAGATATCAG 180
|||||
Db 342 tctgagcatgctctgtctctgtctctgtactctgagcgagatgattcctaagatacag 401
|||||
OY 181 AAGACGACCTACTGCTTTTATAGATTCCTGACACCTCCATGAAAGAGCATTTGAGG 240
|||||
Db 402 aagacgacactactgctcttctatagaaactcgtgagactccatgaagaacgaggttgcagg 461
|||||
OY 241 ACTGACGCTGAGAGGTGAGACACACTACTGACTGCTCTGACGAGATGAAACAGCT 300
|||||
Db 462 actgacgctgagaggtgagagacactactgactgctctgagagaggttgaacaagcct 521
|||||
OY 301 TTCAGGGGGCCGTGACAGAGAACTGCAACACATTTGGGGCCACAGCGCTTTCAGAG 360
|||||
Db 522 ttcagggggcccgtgacagagagactgcaacacattgtgaggccacagcgtcttccaggag 581
|||||
OY 361 CTCACGCTATGATGAGAAAGCTCATGTTGAGTGGGCCACAGAGGCAAGCTGAGGCC 420
|||||
Db 582 ctccagctatgataagagctcatagtttgagatgagcccaagagagagcctgagagccc 641
|||||
OY 421 AGCCATTTGCACACCTCACACATCAATGCTGCCAGCATCCATCGGGTCCCATAAATGCA 480
|||||
Db 642 agccatttgcacacctcacatccaatgctgcccagcatcccatcggttcccataagtca 701
|||||
OY 481 CTCTGCTCTTGTGTCACAGATTCAGAGCTGGGCCAAGATCTCTTAACATGACGTTAAACA 540
|||||
Db 702 ctctgctcttgtgtaccacagatcagagctgggccaagatctcttaacatgagttlaagca 761
|||||
OY 541 ACGGAATAAGAGGTTTAACTCAAGATGGCTCTATTACTGTACCCCAACATTTGCTTTC 600
|||||
Db 762 acggaataagaggtttaaactcaagatggctctattactgtaccccaacatttgccttc 821
|||||
OY 601 GGCATCATGAACATCGGGAAGGTACCTACACACTATCTTCAGCTGATGTTGTCG 660
|||||
Db 822 ggcattcatgaacatcggaaggtacctacacactatcttcagctgattgtgtatg 881
|||||
OY 661 TTAANAACAGCATCAAAATCCCAAGTTCATTAACCTGATGTAAGAGGAGGACAGAA 720
|||||
Db 882 ttaanaacagcatcaaaatcccaagttcattacataactgtgaagagagagacagaaaa 941
|||||
OY 721 ACTGTCGGGCAATTCCTGATTCATCTTTATCTCAATATGTGGGATTTTCAAC 780
|||||
Db 942 actgtcgggcaattcctgattcattcttatctcataaatgttgggagattttccaagc 1001
|||||
OY 781 TCCGAGCTGTGAAGAAATAGATTCAGTGTCCAAACCCCTCCCTGCTGATCCGATC 840
|||||
```


Db 1002 tccgagcgtgctgaagaatcagcaltcagtgctccaaacctccctgctgagtcgcgagtc 1061
Qy 841 AAGATCGACGACTACTTTGGGCTTTCAAGATTCAGACATAGACTGACATCAATTTGCTG 900
Db 1062 aagatgagacgactcttggtgcttcaaaagctcagacatagacagacacacacacacacac 1121
Qy 901 GAACATTAGCATGATGCTCAGATGTTTGGAACTTCTTAAAAATGATGATGATGAT 960
Db 1122 gaacattagcatgagctcagacagctcagacagctcagacagctcagacagctcagac 1181
Qy 961 ACATGTGTAACTACTAAGACATGCGCCACGCTGATGATGATGATGATGATGATGAT 1020
Db 1182 acatgtgtaaactactaagacagctcagacagctcagacagctcagacagctcagac 1241
Qy 1021 TTGAGCCGTGACAGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1242 ttgagccgtgacagttgtgattgattgattgattgattgattgattgattgattgattg 1301
Qy 1081 TACACAAAGGTTTACAAATTTTGAATGATTTCTAGATTTGAACAGATTTGGAGAGGT 1140
Db 1302 tacacaaaggcttacaattctgtaattctcctagaaatcgaaacagattggagaggt 1361
Qy 1141 ATTCCGATGCTTATGAAAAATTACAGTGTAGCTATGAGAGGGCTCAGACTCTGCGGT 1200
Db 1362 attccgatgcttattgaaaaattacagtgtgactatgaaagggttcacagctcctggt 1421
Qy 1201 CTAACCCCTGGACATGTCGCACTGAGAACCTTGAATTAAGAGATGCGCATGCTATGCA 1260
Db 1422 ctaacccctggacatgtcgcactgagaaacctgaaatlaaaggatgacagatcagtcgca 1481
Qy 1261 AAGAAATCATAGTGTGAAGGCTTAACTTTGAATTTGATTTGATTTGATTTGATTTG 1320
Db 1482 aagaaatcatagtggtgaaggcttaaactttgaatttgaattgtaacttgagctgagccctgc 1541
Qy 1321 AAATAAGTCTTTTCTTCTATGAGAGAGAAAAATATATATTTTATATATATGCTA 1380
Db 1542 aaataagtcttttcttctatgagagagaaaaatataatatttataataatgctta 1601
Qy 1381 AAGTATATTTTCACTGATGTTTCTGTCGCAAGTTTGTAAATTAATTAATTTGCTAT 1440
Db 1602 aagtataatttcaactgagtgtaagcttctctgtaaaagtttgaataatatttctgctat 1661
Qy 1441 AGTATTTGATTTCAAAATATTTTAAATGCTCTACTGTTGACATATTTTAATGTTTAAATG 1500
Db 1662 agtatttgaatttcaaaaattttaaataatgctcactgtgacataatttaatttaaatg 1721
Qy 1501 TACAGATGATTTAACTGCTGCACTTTGTAATTCCTGTAAGGTAACCTGTAAGGAGG 1560
Db 1722 tacagatgattttaaactgctgcaacttctgtaattccctgaaagtaactgtaagggg 1781
Qy 1561 GCAGAACTACTGTTTCTGTCGACACATAGTATGTTTATTTCTTTTAACTTATA 1620
Db 1782 gcagaaactactggttctgctgacacatagttatttcttcttcttcttcttcttctt 1841
Qy 1621 GAGTCTTACG 1630
Db 1842 gagtcttctcag 1851

RESULT 6
US-08-989-362-1
Sequence 1, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens: Related
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 125..1072
US-08-989-362-1

Query Match 99.1%; Score 1615.8; DB 4; Length 2191;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CCGGCGTCCACACAGAGGTCGCTGACACCCGCGCTTGTGACCGCGCTCCGGCGCCG 60
Db 189 CCGGCGTCCACACAGAGGTCGCTGACACCCGCGCTTGTGACCGCGCTCCGGCGCCG 248
Qy 61 CACCGCGCGCTCCGCTCCATGTTCTGCGCCCTCTGGGGCTGGAGCTGGCCAGGTG 120
Db 249 CACCGCGCGCTCCGCTCCATGTTCTGCGCCCTCTGGGGCTGGAGCTGGCCAGGTG 308
Qy 121 TCTGACGATCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 309 TCTGACGATCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
Qy 181 AAGACACACTCACTGCTTTTATGAACTCTGAGACTTCATGAAAGCGCAGATTTGAGG 240
Db 369 AAGACACACTCACTGCTTTTATGAACTCTGAGACTTCATGAAAGCGCAGATTTGAGG 428
Qy 241 ACTGACTGTGAGAGTGAAGACACACTGACTGACTGCTGCTGAGAGAGTGAAGAGCT 300
Db 429 ACTGACTGTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 488
Qy 301 TTCAGGGGCGGTGACAGAGAACTGCACACATTTGGGGCCACAGCGCTTCTCAGAG 360
Db 489 TTCAGGGGCGGTGACAGAGAACTGCACACATTTGGGGCCACAGCGCTTCTCAGAG 548
Qy 361 CTCAGCTATGATGAGAGGCTGATGTTGATGTTGAGGCTGAGGCGCAGAGAACCTGAGG 420
Db 549 CTCAGCTATGATGAGAGGCTGATGTTGATGTTGAGGCTGAGGCGCAGAGAACCTGAGG 608
Qy 421 AGCCATTGACACCTCACCATCAATGCTGCCAGCATCCATGGGTTCCCATTAAGTCA 480
Db 609 AGCCATTGACACCTCACCATCAATGCTGCCAGCATCCATGGGTTCCCATTAAGTCA 668
Qy 481 CTCTGTCTTGTGGTACACGATCGAGGCTGGGCGCAAGATCTTAACATGACGTTAAGCA 540

Db 669 CTCTGTCCTTGGTACACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGCA 728
QY 541 ACGGAAACCTAAGGGTTAACCAGATGGCTTCTATTACCTGTAACGGCAACATTTGCTTC 600
Db 729 ACGGAAACCTAAGGGTTAACCAGATGGCTTCTATTACCTGTAACGGCAACATTTGCTTC 788
QY 601 GGCATCATGAACATTCGGGAAGGCTACACATCATCTTCAGAGCTGATGATGTCG 660
Db 789 GGCATCATGAACATTCGGGAAGGCTACCTACAGCATCTTCAGAGCTGATGATGTCG 848
QY 661 TTTAAACACGATCAAAATCCCAAGTTCTCATTAACGTATGAAGAGGAGCAGCAAAA 720
Db 849 TTTAAACACGATCAAAATCCCAAGTTCTCATTAACGTATGAAGAGGAGGAGCAGCAAAA 908
QY 721 ACTGTGGGGAATTCGAAATTCACCTTTATTCCTAATATGTTGGGGGATTTTCAAGC 780
Db 909 ACTGTGGGGAATTCGAAATTCACCTTTATTCCTAATATGTTGGGGGATTTTCAAGC 968
QY 781 TCCGAGCTGTGAAGAAATTTAGCATGAGTGTCCAAACCTTCCTGCTGATCCGGATC 840
Db 969 TCCGAGCTGTGAAGAAATTTAGCATGAGTGTCCAAACCTTCCTGCTGATCCGGATC 1028
QY 841 AAGATGCGAGCTACTTGGGCTTCAAAAGTTCAGGACATAGACTGAGACTCATTTGCTG 900
Db 1029 AAGATGCGAGCTACTTGGGCTTCAAAAGTTCAGGACATAGACTGAGACTCATTTGCTG 1088
QY 901 GAACATTAGCATGATGCTCAGATGTTGGAACTTCTTAAAAATGATGATGCTCAT 960
Db 1089 GAACATTAGCATGATGCTCAGATGTTGGAACTTCTTAAAAATGATGATGCTCAT 1148
QY 961 ACATGTGTAAAGCTACTTAAGAGACATGGCCACGGGTATGAAAACGACAGCCCTCTCTC 1020
Db 1149 ACATGTGTAAAGCTACTTAAGAGACATGGCCACGGGTATGAAAACGACAGCCCTCTCTC 1208
QY 1021 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGCTATGTATATCATGCTAT 1080
Db 1209 TTGAGCCTGTACAGGTTGTATATGTAAAGTCCATAGCTATGTATATCATGCTAT 1268
QY 1081 TACACAAAGGTTTACATTTTGTATATGATTTCCCT-AGAAATTGAACGATTTGGAGAG 1139
Db 1269 TACACAAAGGTTTACATTTTGTATATGATTTCCCTAAGAAATTGAACGATTTGGAGAG 1328
QY 1140 TATTCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGTCACAGTCTCTGG 1199
Db 1329 TATTCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGTCACAGTCTCTGG 1388
QY 1200 TCTAACCCCTGGACATGTCGCCACGTAGAACCTTGAATTAAGAGATGCATGCTATGC 1259
Db 1389 TCTAACCCCTGGACATGTCGCCACGTAGAACCTTGAATTAAGAGATGCATGCTATGC 1448
QY 1260 AAAGAAATGATAGTGTGAAGGGTAAAGTCTTTGAAATTTGATACATTCGCTGGAGCTG 1319
Db 1449 AAAGAAATGATAGTGTGAAGGGTAAAGTCTTTGAAATTTGATACATTCGCTGGAGCTG 1508
QY 1330 CAATTAAGTCTTTTCTTAATGAGAGAGAAAAATATGATATTTTATATATGCTCT 1379
Db 1509 CAATTAAGTCTTTTCTTAATGAGAGAGAAAAATATATATTTTATATATGCTCT 1568
QY 1380 AAAGTATATTTTACAGTGAATGTTCTGTCGCAAAAGTTTGTAAATTAATTTGGCTA 1439
Db 1569 AAAGTATATTTTACAGTGAATGTTCTGTCGCAAAAGTTTGTAAATTAATTTGGCTA 1628
QY 1440 TGAATTTGATTCAAAATATTTAAAAATGTCACGTGTGACATATTTAATGTTTAAAT 1499
Db 1629 TGAATTTGATTCAAAATATTTAAAAATGTCACGTGTGACATATTTAATGTTTAAAT 1688
QY 1500 GTACAGATGATTTAACTGTCGACCTTTGTAATCCCTGGAAGTACTGTAGCTAAGGG 1559
Db 1689 GTACAGATGATTTAACTGTCGACCTTTGTAATCCCTGGAAGTACTGTAGCTAAGGG 1748
QY 1560 GGCAGAAATCTTTTCTGTCGACCATGTAGTTATTTCTTATCTTTTAACTTAAT 1619
Db 1749 GGCAGAAATCTTTTCTGTCGACCATGTAGTTATTTCTTATCTTTTAACTTAAT 1808

QY 1620 AGAGTCTTCAG 1630
Db 1809 AGAGTCTTCAG 1819

RESULT 7
US-09-521C-3
; Sequence 3, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (185)..(1135)
US-09-521C-3

Query Match 57.6%; Score 939.6; DB 4; Length 2271;
Best Local Similarity 78.1%; Pred. No. 4,5e-247;
Matches 1285; Conservative 0; Mismatches 314; Indels 47; Gaps 11;

QY 1 CCGGCGTCCACAGAGGGTCCGCTGCACCCCGGCTTCGACCGGGCTCCGGCGCGC 60
Db 249 ccggagcccgccagagggcccgctgcaccccgcttcgacccggctccggcgcgccagc 305
QY 61 CACCGCGGCTCCCGGCTCCATGTTCTGCGGCTCTGCGGCTGGAGCTGGGCCAGGTGG 120
Db 306 ccccgccgctcccgccgctccatggttcgtgagcgcagatggatccttaacgatttcag 365
QY 121 TCTGACAGATGCTGCTGTTCTGTACTTTCGACGCGAGATGGATCTTAACGAAATATCAG 180
Db 366 tctgacagctgcctgttctgtacttttcgacgcgagatggatccttaacgatttcag 425
QY 181 AAGACAGACACACGCTTTATATGAAATCTGAGACTCATGAAAAACGACATTTGCAGG 240
Db 426 aagatgacacacacgctttatataaattctgagactcatgaaaaacgacatttcag 485
QY 241 ACTGCAGCTGTGAGAGTGAAGACAC-----ACTACCTGACTCTCTGACGAGATGAAC 294
Db 466 acacacactcgtgagagtcataagaataaataataacactgattcatgtagaattaaac 545
QY 295 AAGCTTTTCAGGGGCGCTGCAAGAAAGTGCACACATATGTGGGGCGCACAGGCTTCT 354
Db 466 aagcctttcagggcgctgcaagaaagtgcacacatattgtggggcgcacaggcttct 605
QY 546 aggcctttcagagagctgtgcaaaagaaattacaacatattgtgagatcacagcacatca 605
Db 355 CAGGAGCTCCAGCTATGATGGAAGGCTGATGATGATGATGATGATGATGATGATGATG 414
QY 606 gagcagagaagaagcagatgtgagatgctcattgagatcagcagagagagagcagctg 665
Db 415 AGGCCAGCCATTTTGCACACCTCACCATCATGCTGCGACATCCCATGGGTTCCCTA 474
QY 666 aagccagccttttgctcattcactatcattatgaccagcagcagcagcagcagcagc 725
Db 475 AAGTCACTGTGCTCTTGTGTCACAGATCGAGGCTGGGCGCAAGATCTTAACATGAGAGT 534
QY 726 aagtgagctgtcctcttctgtacacatgacgagtggttgagcagagatcccaacagact 785
Db 535 TAAGCAGCGAAGAAATAAGGTTTAACCAAGATGCTTCTATTACTGTAGCGCAACATTT 594

Db 786 ttaagcaatggaacaaacaaagtaacaaagatcgagatcgcttattactgtatgcaacattt 845
OY 595 GCTTTCGCGCATGATGAAACATCGGGAAGCGTACTACAGACTATCTTACGTGATGTGT 654
Db 846 gcttcgacatacatgaacttccaggaacctgacacagagatattctaaccaatggtgt 905
OY 655 ATGTGCTTAAACACAGACTCAAAATCCCAAGTTCATTAACCTGATGAAGAGGAGACA 714
Db 906 agctaacataaaacacgacatacccaagttctcaatacctgattgaagaagaaga 965
OY 715 CGAAAAACGTCGCGCAATTCGAAATTCGCAATTCATTAATGATGGGGATTTT 774
Db 966 ccaagatattggtcgaaggaaatctcgaaatcttattcctcaaaacgttggatattt 1025
OY 775 TCAAGCTCGAGACTGGTGAAGAAATTAAGCATTCAGGTGTCAACCCCTCCCTGAGATC 834
Db 1026 ttaagttacggtctcgaggagaaatcagacatcgaggtctccaaacccctctacgtatc 1085
OY 835 CGGATCAAGATCGCAGCTACTTGGGCTTTCAAAGTTCAGGACATAGACTGAGACTGAT 894
Db 1086 cggatcagagatgcaacatacttgggtctttaaagttcgaagataagatcgagccag 1145
OY 895 TTCGTGAACAATTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 947
Db 1146 tttttggaggtgtt---agttattcccgagagttcgaaacatttctaaacaaagccaa 1202
OY 948 GGATGATGCTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1007
Db 1203 gaaagatgataatgagtggtgagacttaagagagcatgcccacaaagagacagatc 1262
OY 1008 ACAGCCCTCTCTCTGAGACCTGTACAGTGTGTATATGATTAAGTTCATAGTATGTTA 1067
Db 1263 agtaccatgctctgacacctgtagaagacagcgatcttcaagccagtgagaggttla 1322
OY 1068 GATTGATGCTG-ATTACACAAGGTTTACAAATTTGTATGATGATGATGATGATGATGAT 1126
Db 1323 gactcaatggtgttaccacaaatggtttaaatttctgaatctccaaatlaaac 1382
OY 1127 AGATGCGAGAGAGTATTCGATGCTTATGAAAACCTACAGTGAATGGAAGGGGT 1186
Db 1383 agatcgagacaaatcagaggttgcaccttaagaaactgacatggtgagagaggt - 1440
OY 1187 CACAGTCTCTGGGTACACCCCTGACATGTCGCCACTGAGAACCTTGAAATTAAGAGAT 1246
Db 1441 -----tggctccctggttcccttgcagc-tgaagtgagagaggt 1485
OY 1247 GCGATGCTATGCAAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1306
Db 1486 gtacatct-aggcacaatgaaagatcactcgaaggagcaaatcttctgaattgtacatc 1544
OY 1307 GCGCTGGGACCTGCAAAATAGTCTTTTCTTATGAGAGAGAAAATATATGATTT 1366
Db 1545 atgctggaacctgcaaaaaaac--tttctcaatgagagag-aaaaatcgtatctt 1600
OY 1367 TTAATATATGCTAAAGTATATATTAAGTATGATGATGATGATGATGATGATGATGAT 1426
Db 1601 ttataataatacctaagttataatctcagaatgaaatgttcttctgcaaaagatgttaaat 1660
OY 1427 TATATTTGCTATAGTATTTGATTTCAAAATATTTAAATATGCTGATGATGATGAT 1486
Db 1661 tataattgtctatagatatttgatcacaataatcttaaaaaatgcttctgttgcataatc 1720
OY 1487 TAAATGTTTAAATGATACAGATGATTTTAACTGTCGACTTTGTAATTCCTG-AAA 1541
Db 1721 taatgttttaaaatgtaagaaatcttaaacgtgcaacttgcataatccctgggaa 1780
OY 1542 GGTACTGCTACCTAAGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1601
Db 1781 ctgctcagctaaaggaggaagaaatgcttcttccataatacaaatgcagatattctt 1840
OY 1602 TATTTCTTTTAACTTAATAGAGTCTT 1627
|||||

Db 1841 cgtctctttaaagtaataatattt 1866
RESULT 8
US-08-996-139-12
; Sequence 12, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 954 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: huRANKL (full length)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-996-139-12
Query Match 37.7%; Score 615; DB 3; Length 954;
Best Local Similarity 82.2%; Pred. No. 1,4e-158;
Matches 734; Conservative 0; Mismatches 150; Indels 9; Gaps 2;
OY 1 CCGGCGTCCACAGAGAGGTCCGTCGACCCGCGCTTCTGACGCGGTCCGAGCGCG 60
Db 65 CCGGAGCCCGCAGAGAGGCGCCCTGACGCGCCCGC---CCCGCGCTGCGCGCACG 121

QY	61	CA	CCCGCCGCTCCCGCTCCATGTTCTCTGGCCCTCTCGGGGCGTGGGACATCGGGCCAGGTGG	120
Db	122	CCCCCGCGGCTCCCGCTCCATGTTCTGGCCCTCTCGGGGCGTGGGCGTGGGCGAGTTGG	181	
QY	121	TC	TGACAGATCGGCTCTGCTTCCTGACTTTTGAGCGGAGATGATTCCTTAACAGAAATTCAG	180
Db	182	TC	TGACAGGTGCGCCCTTTCTTCTATTTCAGACGCGAGATGATTCCTAAATGATTCAG	241
QY	181	AA	GACAGACTCACTGCTTTTATAGAAATCTGAGACTCCATGAAACGCAGATTTGCAAG	240
Db	242	AA	GTGAGACTCACTGCAATTTATAGAAATTTGAGACTCCATGAAATTCGAGATTTTCAAG	301
QY	241	AC	TGACTCTGGAACATGGAACAC-----ACTACTGACTCTCGAGGAGGATGAAAC	294
Db	302	AC	ACAACTCTGGAAGTCAACATTCAAAATTAATACCTGATTCATGAGAGATTTAAAC	361
QY	295	AA	GCTTTTCAGGGGGCCGTGAGAAAGGACTGCACACATTTGTGGGCGCACAGCGTTCT	354
Db	362	AG	CGCTTTTCAGAGAGCTGTGCAAAAGATTTACAACTATTCGTTGGATTCACAGCACTCA	421
QY	355	CA	GAGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCGACGAGCAAGCTTG	414
Db	422	GA	GAGCAGAAAGCGATGGTGGATGGCTCATGTTAGATTCGGCCAAAGGAGCAAGCTTG	481
QY	415	AG	CGCCAGCATTTGTCACACTCACTCACTCATGCTGGCAGATCCCATGGGGTTCCATA	474
Db	482	AA	GCTCACACTTTCCTTCATCTACTATTAATGACCCGACGATCCCATCTGGGTTCCATA	541
QY	475	AA	GTCATCTGCTCTTGGTACACAGATCGAGGCTGGGCGCAAGATCTCAACATGACGT	534
Db	542	AA	GTAAGTCTGCTCTTGGTACATGATCGGGGTTGGGCGCAAGATCTCAACATGACTT	601
QY	535	TA	AGCAAGGAAACCTAAGGCTTAACCAAGATGCTCTTATTTACCTGTAGCCACACTT	594
Db	602	TA	AGCAATGAAAACTAATAGTTATTCAGATGAGCTTATTTATTCCTGTATGCCAACTT	661
QY	595	GC	TTTCGCTATATAAATCTCGGAACGATACCTACAGACTATCTCAGCTGATGGTGT	654
Db	662	GC	TTTCGATCATATAAATCTCGGAACGATACCTACAGACTATCTCAGCTGATGGTGT	721
QY	655	AG	TGCTTAAACACAGCATCAAAATCCCAAGTTCATATACCTGATGAAAGAGGAGACA	714
Db	722	AG	CTCACTAAACAGCATCAAAATCCCAAGTTCATATACCTGATGAAAGAGGAGACA	781
QY	715	CG	AAATCTGTGCGGCAATTCGATTCACATTTATTCATAAATGTTGGGGATTTT	774
Db	782	CG	AAGTATGTGCAGGGAATTCGATTCACATTTATTCATAAATGTTGGGGATTTT	841
QY	775	TC	ACGCTCGGAGCTGCTGAAGAAATTAGATTCAGGTCGCAACCTTCCTCGCTGATC	834
Db	842	TA	AGTATGAGGTCTGAGAGGAAATCAGATGAGGTCCTCAACCTTCCTTACTGATC	901
QY	835	CG	AGTAAAGTGCAGCTACTTTGGGGCTTTCAAAGTTTCAGACATATGACGA	887
Db	902	CG	AGTAAAGTGCAGCTACTTTGGGGCTTTCAAAGTTTCAGATATATGATTGA	954
RESULT 9				
US-08-995-659-12				
; Sequence 12, Application US/0895659				
; Patent No. 6242213				
; GENERAL INFORMATION:				
; APPLICANT: Anderson, Dirk M.				
; APPLICANT: Galibert, Laurent				
; APPLICANT: Marasovsky, Eugene				
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappab				
; NUMBER OF SEQUENCES: 19				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Immunex Corporation, Law Department				
; STREET: 51 University Street				
; CITY: Seattle				
; STATE: WA				
; COUNTRY: USA				

```

1 ZIP: 98101
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Floppy disk
4 COMPUTER: Apple Power Macintosh
5 OPERATING SYSTEM: Apple Operating System 7.5.5
6 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/995,659
9 FILING DATE: 22 DECEMBER 1997
10 CLASSIFICATION:
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US95N 60/064,671
13 FILING DATE: 14 OCTOBER 1997
14 CLASSIFICATION:
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US95N 08/813,509
17 FILING DATE: 07 MARCH 1997
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US95N 08/772,330
21 FILING DATE: 23 DECEMBER 1996
22 CLASSIFICATION:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Perkins, Patricia Anne
25 REGISTRATION NUMBER: 34,693
26 REFERENCE/DOCKET NUMBER: 2852-A
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (206)587-0430
29 TELEFAX: (206)233-0644
30 INFORMATION FOR SEQ ID NO: 12:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 954 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA
37 HYPOTHETICAL: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 ORGANISM: Homo sapiens
41 IMMEDIATE SOURCE:
42 LIBRARY:
43 CLONE: hURANKL (full length)
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 1..951
47 US-08-995-659-12
48
49 Query Match 37.7%; Score 615; DE 4; Length 954;
50 Best Local Similarity 82.2%; Pred. No. 1,4e-158;
51 Matches 734; Conservative 0; Mismatches 150; Indels 9; Gaps 2
52
53 1 CCGGCGTCCCAACAGAGGTCGCGTCGACCCCGCGCTTGTGGACCGGCGTCCGCGCCGCG 60
54 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
55 CCGGAGCCCGGACAGAGGCGCCCTCGACGCCCCGCG--CGCCGCGTCGGCCGACACAGC 121
56
57 61 CACCGCGCGGCTCCCGCTCCATGTTCTGGCCCTCCTGGGCGTGGAGACTGGGCCAGGTG 120
58 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 122 CCCCCCGCGCTCCGCTCATGTTGCTGCGCCCTCTGGGGCGTGGGCGTCAGGTTG 181
60
61 121 TCTGACAGCATGCTGTGTTCTGTACTTTCGAGCGCAGATGATCTTAACAGATTCAG 180
62 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
63 182 TCTGACAGCGTCCGCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGATATCAG 241
64
65 181 AAGACAGCATCTACTGCTTTATAGAACTCTGAGACTCCATGAAAAATGCAGATTTTCAAG 240
66 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 242 AAGATGGCACTCACTGATTATAGAAATTTTGAGACTCCATGAAAAATGCAGATTTTCAAG 301
68
69 241 ACGTCGATCTGGAGAGTGAAGACAC-----ACTACCTGACTCCTGCAGAGGATGAAC 294
70 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
71 302 ACGACACTCTGGAGAGTGAAGTACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 361
72

```

QY	295	AAGCCTTTACAGGGGGCCCTGCGAGAAAGAAATGCAACACATTTGTGGGGCCACAGGGCTTCT	35
Db	362	AGGCCCTTTCAGAGAGCTGTGCAAAAGGAATTACACATATCTTTGGATCACAGACATCA	422
QY	355	CAGGAGCTTCAGACTATGATGGAAGGCTTCATGTTGGATGTGGCCAGGAGCAAGCCTG	414
QY	415	AGGCCACCCATTGGCCAACTCACCATCATTCGTGCCAGATCCCATCGGGTTCCATA	474
Db	422	GAGCAGAGAAAAGCCGATGGTGGATGGCTCATGTTAGATCTGGCCAAAGGAGCAAGCTTG	481
QY	442	AGGCTACACCTTTTGCTATCTATCTATTAATGACACGACATCCCATGTGGTCCATA	541
QY	475	AAGTCACTCTGTCCTCTTGGTACCAAGATCGAGGCTGGGCCAAGATCTCTAACTAGAGT	534
Db	542	AAGTAGCTGTGCTCCTTGTAACATGATTCGGGGTTGGGCCAAGATCTCCAACTAGACTT	601
QY	535	TAAAGCAACGGAAAACTAAGGGTTAAACCAAGTGGCTTCTATTACCTGTAGCCACACTTT	594
Db	602	TTAGCAATAGGAAAACATAATTAATCTAATACGATGGCTTTTATTAACCTGTATGGCCAACTTT	661
QY	595	GCTTTCGGCATCATGAAACATCGGGAAGCCGATACAGACTATCTTCAGCTGATGGTGT	654
Db	662	GCTTTGCACATCATGAAACTTCAGAGAGCCTTAGCTACAGAGATCTTCAACTAATGGTGT	722
QY	655	ATGTGCTTAAACACAGCATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGGAGACA	714
Db	722	AGCTCACTAAACACGCAATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGAGACA	781
QY	715	CGAAAACCTGGCGGGCACTCTCAATTCGACTTTATTCATTAATAGTTGGGGGATTTT	774
Db	782	CCAGGATATTGGTCAGAGGAAATCTCAATTCATTTTATTCATTAACCTGTGGTGATTTT	841
QY	775	TCAGAGCTTCGAGCTGGTGAAAGAAATTAGCATTCAGGTGTCCAAACCTTCCCTGCTGATC	834
Db	842	TTAAGTTACGGCTGTGGAGAGAAATCAGCATCGAGGTCTCCAAACCTCCCTTACTGGATC	901
QY	835	CGGATCAAGATGCCAGCTACTTTGGGGCTTTCAAAGTTTCAGAGCATAGACTGA	887
Db	902	CGGATCGAGATGCAACATCACTTTGGGGCTTTTAAAGTTGAGATATGATTGA	954
RESULT 10			
US-09-215-649A-12			
Sequence 12, Application US/09215649A			
Patent No. 6271349			
GENERAL INFORMATION:			
APPLICANT: Anderson, Dirk M.			
Galibert, Laurent			
Marasovsky, Eugene			
TITLE OF INVENTION: Receptor Activator of NF-kappaB			
NUMBER OF SEQUENCES: 19			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Immunex Corporation, Law Department			
STREET: 51 University Street			
CITY: Seattle			
STATE: WA			
COUNTRY: USA			
ZIP: 98101			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: Apple Power Macintosh			
OPERATING SYSTEM: Apple Operating System 7.5.5			
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/215,649A			
FILING DATE: 17-Dec-1998			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/996,139			
FILING DATE: <Unknown>			
APPLICATION NUMBER: USN 08/813,509			
FILING DATE: 07 MARCH 1997			
APPLICATION NUMBER: USSN 08/772,330			

```

1      FILING DATE: 23 DECEMBER 1996
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Perkins, Patricia Anne
4      REGISTRATION NUMBER: 34,693
5      REFERENCE/DOCKET NUMBER: 2851-A
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (206)587-0430
8      TELEFAX: (206)233-0644
9      INFORMATION FOR SEQ ID NO: 12:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 954 base pairs
12     TYPE: nucleic acid
13     STRANDEDNESS: single
14     TOPOLOGY: linear
15     MOLECULE TYPE: cDNA
16     HYPOTHETICAL: NO
17     ANTI-SENSE: NO
18     ORIGINAL SOURCE:
19     ORGANISM: Homo sapiens
20     IMMEDIATE SOURCE:
21     LIBRARY: <unknown>
22     CLONE: hurANKL (full length)
23     FEATURE:
24     NAME/KEY: CDS
25     LOCATION: 1..951
26     SEQUENCE DESCRIPTION: SEQ ID NO: 12:
27     US-09-215-649A-12

```

	Query Match	Similarity	37.7%	Score 615	DB 4	Length 954
	Best Local	Similarity	82.2%	Pred. No.1.4e-156		
	Matches	734	Conservative	0	Mismatches	150
					Indels	9
					Gaps	2
QY	1	CCGGGCTCCACACAGAGGGTCCGCTGCACCCCGCCCTCTTCTGCACCGGCTCCGGCGCCG	60			
Db	65	CCGGAGCCCGGAGAGGGCCCGCTGCACCGCCGCGC	121			
QY	61	CACCCGCGCCCTCCCGCTCCATGTTCTCTGGCCCTCTGGGGCTGGGACTGGGCCAGGTGG	120			
Db	122	CCCGCCGCGCTCCCGCTCCATGTTCTGGGGCCCTCTGGGGCTGGGGCTGGGCCAGGTGG	181			
QY	121	TCTGCAGACTGCTCTGTTCCGTACTTTCGAGCCAGATGGATCTTAAAGAAATATAG	180			
Db	182	TCTGCAGGCTGGCCCTGTTCTTCTTATTTTCAGAGCCCAATGATCTCTAATAGAAATATAG	241			
QY	181	AAGACAGACTCTACTGCTTTTATAGAAATCTGAGACTCCATGMAAACGACATTTTGCAGG	240			
Db	242	AAGATGCACTCACGCTATTTATAGAAATTTTGAGACTCCATGMAAAATGACATTTTTCAG	301			
QY	241	ACTGCACTCTGAGAGTAAAGAC-----ACTACCTGACTCTCTGCAGGAGATGAAC	294			
Db	302	ACACAACTCTGAGAGTCAAGATACMAAATTAATACCTGATTAATGAGGAAATTAAC	361			
QY	295	AAGCTTTTCAGGGGGCCCTGCAGAAAGCAACATGATTTGGGGGACAGCGCTTCT	354			
Db	362	AGGCTTTCAAGGAGCTGTGCMAAAGAAATTAACAACATATGCTTGGATCACAGCAATCA	421			
QY	355	CAGAGCTCCAGCTATGATGAGAAAGGCTCATGTTGGATGTGGGCCAGGCAAGCTTG	414			
Db	422	GAGGAGMAAAAGCATGGTGGATGGCTCATGTTAGATCTGTGGCCMAAGAGGACAGCTTG	481			
QY	415	AGGCCACGCCAATTTGCAACACTGCACATCAATGGCTGGCCAGATCCCATGGTTCCCA	474			
Db	482	AAGCTCAAGCTTTTGTCTCATCTCACTATTAATGCAACGACATCCCATCTGTTCCCA	541			
QY	475	AAGTCACTCTGTCTCTTGGTACACAGATCGAGGCTGGGGCAAGATCTTAACATGACGT	534			
Db	542	AAGTGAAGTCTCTCTCTTGGTACCATGATCGGGTGGGGCAAGATCTTAACATGACGT	601			
QY	535	TAAACACGAAATCTAAGGTTAAACCAAGATGGCTTATATTACTGTAGCCCAACATTT	594			
Db	602	TTACCAATGGAATCTAATAGTTAATCAAGATGGCTTATATTACTGTATGCCCAACATTT	661			

US-08-584-031-2
: Sequence 2, Application US/08584031A
: Patent No. 6030945
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: APO-2 LIGAND
: FILE REFERENCE: 11669.22US03
: CURRENT APPLICATION NUMBER: US/08/584, 031A
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1042
: TYPE: DNA
: ORGANISM: Homo sapiens
US-08-584-031-2

Query Match 3.6%; Score 58.4; DB 3; Length 1042;
Best Local Similarity 50.0%; Pred. No. 1.9e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;
QY 525 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
DB 586 aacttgcaacttggaatggtgacactggtcaccatgaaagaggttaccacacatc 645
QY 585 GCCAACATTTGCTTTGGCATCATGAACATCGGACGTAACGACTATCTTCAG 644
DB 646 tcccaaacacacttgcattcagagagaa---ataaagaacaaacaaagacagacaa 702
QY 645 CTGATGCTGATGCTGTTAAACCAACATCAAAATCCCAAGTTCATTAACCTGATGAA 704
DB 703 caaatggtccaaataatctcaaaatacaaaagtcctgacccatattgttgatgaa 762
QY 705 GGAGGACGACGAAACAACTGTCGGCAATTCGAATTCCTAATTCATTAATGTT 764
DB 763 agtgcagagaatagtggtcgtcctaagaatgagaaatagatcctatcctacataa 822
QY 765 GGGGATTTTTCAGCTCCGACGCTGTGAAGAAATTAGCATTCAGGTGCCAACCCTTCC 824
DB 823 ggggggaatttgcagcttaagaagaaatgacagaaatttgcgtcgttaacaaatgagac 882
QY 825 CTGCTGATCCGATCAAGATCGACGTAATTCGAGCTTGGGCTTTCAAAGTT 872
DB 883 ttgatagacatgacatgaagcagcttcttcggggccttctttagt 930

RESULT 14
US-08-780-496-2
: Sequence 2, Application US/08780496
: Patent No. 6046048
: GENERAL INFORMATION:
: APPLICANT: Avi Ashkenazi, Anan Chuntcharapai, Kyung Jin Kim
: TITLE OF INVENTION: Apo-2 Ligand
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Winpatlin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/780,496
: FILING DATE: 08-Jan-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-780-496-2

Query Match 3.6%; Score 58.4; DB 3; Length 1042;
Best Local Similarity 50.0%; Pred. No. 1.9e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;
QY 525 AACATGACGTTAAGCAACGAAACTAAGGTTAACCAAGATGGCTTCTATTACCTGTAC 584
DB 586 AACCTGACCTTGAGGAATGTTGAACCTGTCATCCATGAAAAAGGTTTACTACATCTAT 645
QY 585 GCCAACATTTGCTTTGGCATCATGAACATCGGAGCGCTACTACAGACTATCTTCAG 644
DB 646 TCCCAACATATCTTTCCATTTTCAGAGAGAA---ATAAAGAAACACAAAGAACGACAAA 702
QY 645 CTGATGCTGATGCTGTTAAACCAACGATCAAAATCCCAAGTTCCTAATCACTGATGAA 704
DB 703 CAAATGGCCCAATATATTTTCAATACACAAAGTATCTCAACCTATATTTGATGAAA 762
QY 705 GGAGGACGACGAAACAACTGTCGGCAATTCGAATTCCTAATTCATTAATGTT 764
DB 763 AGTCTGAATTAATTTGTTGTTGAAGATGCAAGAAATGAGCTCTATTCATCTATCAA 822
QY 765 GGGGATTTTTCAGCTCCGACGCTGTGAAGAAATTAGCATTCAGGTGCCAACCCTTCC 824
DB 823 GGGGGAATTTTGAAGCTTAAGAAATGACAGAAATTTTGTCTGTACAAATGAGCAC 882
QY 825 CTGCTGATCCGATCAAGATCGACGTAATTCGAGCTTGGGCTTTCAAAGTT 872
DB 883 TTGATGACATGAGACCATGAAACGAGTTTTCGGGGCCTTTTAACT 930

RESULT 15
US-08-670-354-3
: Sequence 3, Application US/08670354
: Patent No. 5763223
: GENERAL INFORMATION:
: APPLICANT: Steven R. Wiley and
: APPLICANT: Raymond G. Goodwin.
: TITLE OF INVENTION: Cytokine That Induces Apoptosis
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Apple 7.5.2
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/670,354
: FILING DATE: 25-JUN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/496,632
: FILING DATE: 29-JUN-1995
: CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HuAIC-0V
FEATURE:
NAME/KEY: CDS
LOCATION: 78..383
US-08-670-354-3

Query Match 3.6%; Score 58.4; DB 1; Length 1521;
Best Local Similarity 50.0%; Pred. No. 2.3e-06;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;
QY 525 AACATGACGTTAGCAACGAACTAAGGTTAACCAAGATGGCTTCTATTACTGTAC 584
DB 425 AACTTGACCTTGAGGAATGTGTAAGTGCATCCATGAAAGGTTTACTACATCTAT 484
QY 585 GCCACATTTGCTTGGGCACTCATGAACATCGGGAAGCTACCTACAGACTATCTCAG 644
DB 485 TCCCAACATCTTGCATTCAGAGGAA--ATAAAGAAACACAAGAAAGACGACAA 541
QY 645 CTGATGCTATGCTGTAACCAACGATCAAAATCCCAAGTCTCATTAACCTGATGAA 704
DB 542 CAATGCTCAATATATTACAAATACACAAGTATCCCTATATGTGATGAAA 601
QY 705 GGAAGGAGCAGAAAACCTGGGCAATTCGAATTCCTTTATTCATTAATGTT 764
DB 602 AGTCTAGAAATAGTGTGTAAAGATGCAAGATATGACTATATCCATATCAA 661
QY 765 GGGGATTTTCAAGCTCCGAGCTGTGAGAAATATGACATTCAGGTGCCAACCTTC 824
DB 662 GGGGAAATATTGAGCTTAAGAAATGACGAATTTTGTCTGTAAACAATGAGCAC 721
QY 825 CTGCTGATCCGATCAAGATGCGACGTACTTGGGGCTTCAAAAGTT 872
DB 722 TTGATAGCATGACACGAAAGCAGTTTTCGGGGCTTTTATGTT 769

Search completed: July 8, 2002, 20:04:31
Job time: 710 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:04:46 ; Search time 2842.81 seconds
(without alignments)
7738.835 Million cell updates/sec

Title: US-09-865-363-10

Perfect score: 1630

Sequence: 1 CCGCGCTCCACACGAGGT.....TAACCTTAATAGACTCTTCAG 1630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues 27472414

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estdb:*
- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estlin:*
- 5: em_estlin:*
- 6: em_estlin:*
- 7: em_estlin:*
- 8: em_estlin:*
- 9: gb_estl:*
- 10: gb_estl:*
- 11: gb_hic:*
- 12: gb_hic:*
- 13: em_gse_hum:*
- 14: em_gse_hum:*
- 15: em_gse_hum:*
- 16: em_gse_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	506.2	31.1	612	12 BH267783	BH267783 CH230-186
C 2	442.4	27.1	469	9 BB223942	BB223942 BB223942
C 3	441	27.1	475	9 BB637568	BB637568 BB637568
C 4	317	19.4	482	10 BB633100	BB633100 uv73804.Y
C 5	317	19.4	514	10 BE335979	BE335979 us84609.Y
C 6	262.6	16.1	524	12 AO827122	AO827122 HS_5256.B
C 7	247.8	15.2	575	12 AO417854	AO417854 RPCI-11-1
C 8	228.8	14.0	530	9 AA170348	AA170348 ms88911.F
C 9	228.4	14.0	529	12 AO827168	AO827168 HS_5256.B
C 10	205.4	12.6	659	12 AG107545	AG107545 Pan trogl
C 11	192	11.8	419	9 AA504450	AA504450 aa59n12.F
C 12	181.2	11.1	362	9 AV653073	AV653073 AV653073
C 13	165.8	10.2	618	12 AZ834036	AZ834036 2M0116G04
C 14	116	7.1	413	12 AO817650	AO817650 HS_5265.B
C 15	72.2	4.4	276	10 BG203357	BG203357 RST2738
C 16	72.2	4.4	299	10 BG206497	BG206497 RST25946
C 17	70.6	4.3	277	10 BG184205	BG184205 RST3126.A

C 18	70.6	4.3	609	10 BF427340	BF427340 df64e08.Y
C 19	69	4.2	198	10 BG197160	BG197160 RST16397
C 20	69	4.2	321	10 BG212237	BG212237 RST31821
C 21	68.4	4.2	1101	12 CNS00FMC	AL070972 Drosophila
C 22	61	3.7	683	10 BG016736	BG016736 df64e08.x
C 23	60	3.7	1101	12 CNS00396	AL063921 Drosophila
C 24	59.4	3.6	928	12 CNS00DKY	AL071865 Drosophila
C 25	58.4	3.6	618	9 BE042463	BE042463 hc22c06.x
C 26	58.4	3.6	683	9 AW949689	AW949689 EST361759
C 27	58.4	3.6	718	9 AW945165	AW945165 EST361358
C 28	58.4	3.6	973	9 AL547417	AL547417 AL547417
C 29	58.4	3.6	1055	9 AL543620	AL543620 AL543620
C 30	58.4	3.6	1101	12 CNS00EVL	AL069706 Drosophila
C 31	58.2	3.6	1203	12 CNS015WU	AL106008 Drosophila
C 32	57.2	3.5	907	10 BM581116	BM581116 CA_Fa000
C 33	56.6	3.5	1184	12 CNS04PAP	AL300850 Tetradon
C 34	56.2	3.4	1101	12 CNS00EWT	AL069847 Drosophila
C 35	56	3.4	775	10 BG216814	BG216814 RST36509
C 36	55.6	3.4	524	12 CNS01090	AL167541 Tetradon
C 37	55.6	3.4	647	10 BM440311	BM440311 p91n.pk0
C 38	55.4	3.4	976	12 CNS04F5M	AL286627 Tetradon
C 39	54.6	3.3	945	12 CNS04DOK	AL285169 Tetradon
C 40	54.2	3.3	606	10 BG112984	BG112984 p91n.pk0
C 41	54.2	3.3	1101	12 CNS00KAE	AL077628 Drosophila
C 42	54	3.3	862	12 CNS029ER	AL187164 Tetradon
C 43	54	3.3	988	12 CNS0072R	AL066743 Drosophila
C 44	54	3.3	1063	12 CNS07A2Y	AL436064 T3 end of
C 45	53.8	3.3	585	9 AM104819	AM104819 x057b10.x

ALIGNMENTS

RESULT 1
LOCUS BH267783/c 612 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-186C1, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH267783
VERSION BH267783.1 GI:17180093
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Murinae;
Rattus.
1 (bases 1 to 612)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcORI segment
Unpublished (1999)
Other_GSSs: CH230-186C1.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdjong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_eirng_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 186 row: C column: 1
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..612
/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"

FEATURES

source

```

/db.xref="taxon:10116"
/clone="CH230-186C1"
/clone_id="CHOR1-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/notes="Vector: PTABAC2.1; Site:1: EcoRI;
CHOR1-230 Rat (BN/SENHsd/MCM) BAC library produced by
Pieter de Jong"

```

Query Match	31.1%	Score 506.2;	DB 12;	Length 612;
Best Local Similarity	91.6%	Pred. No. 6.7e-96;		
Matches 547; Conservative	0;	Mismatches 48;	Indels 2;	Gaps 1;

TITLE
JOURNAL
COMMENT

Hiramoto, H., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, K., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashida, Y.

RIKEN Mouse ESTs (Arikawa, T., et al. 2001)

Unpublished (2001)

On Jul 1, 2000 this sequence version replaced gi:8692554.

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

Email: genome-resesc-riken.go.jp/
URL: http://genome.gsc.riken.go.jp/Carninci_P_Shibata_Y_Hayatsu_N_Sugahara_Y_Shibata_K_Itoh_M_Kono_H_Okazaki_Y_Muramatsu_M_and_Hayashizaki_Y
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Itoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

Komoto, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashizaki, Y. (2000) RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 261-269 (2001)

Kondo, S., Shilagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome, 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

source

Location/Qualifiers
1. .469

/organism="Mus musculus"

```
/db_xref="taxon:10090"
```

```
/clone="A530084G16"
```

```
/clone_lib="RIKEN full-length enriched, adult male aorta
```

and vein"

```
/sex="male"
```

/tissue_type="aorta and vein"

```
/dev_stage="adult"
```

```
/lab host="DH10B"
```

/note="Site 1: Sali; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory

Division of Experimental Animal Research in Riken

contributed to prenatal mouse tissues. 1st strand cDNA

primed with a primer [5',
concluded to prepare mouse tissues: 1st strand con

primed with a primer 1) 3' - CDN

prepared by using trehalose thermo-activated reverse

prepared by using Crelasec reverse transcriptase and subsequence for full-length

transcriptase and subsequently enrolled for full-length

cap-trapper. CDNA went through one round of normal 12

to ROT = 20.0 and subtraction to ROT = 459.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTATCCCCCCC

3']. cDNA was cleaved with XhoI and BamHI. Vector: a

ORIGIN

Query Match 19.4%; Score 317; DB 10; Length 514;
Best Local Similarity 100.0%; Pred. No. 3e-56;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1314 GACCTGCAATATAGCTCTTTTCTTAATGAGAGAGAAAAATATATGATTTTATATA 1373
DB 1 GACCTGCAATATAGCTCTTTTCTTAATGAGAGAGAAAAATATATGATTTTATATA 60

QY 1374 ATGCTAAAGTATATATGAGTGTATATCTTCTGTCGCAAGTTTGTAAATATATTT 1433
DB 61 ATGCTAAAGTATATATGAGTGTATATCTTCTGTCGCAAGTTTGTAAATATATTT 120

QY 1434 GTGCTATAGTATATGATTCACAAATATTTAAAAATGTCACGTGACATATTTATGTT 1493
DB 121 GTGCTATAGTATATGATTCACAAATATTTAAAAATGTCACGTGACATATTTATGTT 180

QY 1494 TTAATATGACAGATATTTAACTGTCGACCTTTGTAATCCCTGAAGGTACTGAGC 1553
DB 181 TTAATATGACAGATATTTAACTGTCGACCTTTGTAATCCCTGAAGGTACTGAGC 240

QY 1554 TTAAGGGGAGAAATCTCTTCTGTCGACCAATGATATTTCTTATCTTTTAA 1613
DB 241 TTAAGGGGAGAAATCTCTTCTGTCGACCAATGATATTTCTTATCTTTTAA 300

QY 1614 CTTAATAGAGCTTCAG 1630
DB 301 CTTAATAGAGCTTCAG 317

RESULT 6
LOCUS A0827122/c 524 bp DNA linear GSS 27-AUG-1999
DEFINITION HS 5256.B2.C09.T7A.RPCI-11 Human Male BAC library Homo sapiens
ACCESSION A0827122
VERSION A0827122.1 GI:5793184
KEYWORDS GSS.

SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS Mahalinas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahalinas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

EMAIL: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering-bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.hpsc.washington.edu
Plate: 832 row: F column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 524.

FEATURES
SOURCE 1..524
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="Plate-832 Col-18 Row-F"
/clone_id="RPCI-11 Human Male BAC library"
/sex="male"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI.
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 154 a 116 c 99 g 151 t 4 others
ORIGIN

Query Match 16.1%; Score 262.6; DB 12; Length 524;
Best Local Similarity 73.7%; Pred. No. 7.6e-45;
Matches 375; Conservative 0; Mismatches 123; Indels 11; Gaps 3;

QY 611 AACATCGGGAACCGTACCTACAGACTATCTTACGTATGCTGTTAAACAG 670
DB 521 AGCTTCAGAAACCGTACCTACAGACTATCTTACGTATGCTGTTAAACAG 462

QY 671 CATCAAAATCCCAAGTCTCATTAACCTGATGAAGAGGAGGAGCAAAACCTGTCGG 730
DB 461 CATCAAGATCCCAAGTCTCATTAACCTGATGAAGAGGAGGAGCAAAACCTGTCGG 402

QY 731 CAATTCGAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGCTCCGAGCTGG 790
DB 401 AAATATGAATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGCTCCGAGCTGG 342

QY 791 TGAAGAAATTTGACATTCAGGTGTCACACCTTCCCTGTCGATCCGATCAAGATGCGAC 850
DB 341 AGAGGAATTCAGATTCAGGTGTCACACCTTCCCTGTCGATCCGATCAAGATGCGAC 282

QY 851 GTACTTGGGGCTTTCACAAATGTCAGACATGACATGACATTCGTCGACATATGAC 910
DB 281 ATACTTGGGGCTTTCACAAATGTCAGACATGACATGACATTCGTCGACATATGAC 223

QY 911 ATGATGTCCTAGATGTTTGGAAACTTCTTAAAAAT-----GAGATGATGCTATACA 963
DB 224 ATGATGTCCTAGATGTTTGGAAACTTCTTAAAAAT-----GAGATGATGCTATAGG 165

QY 964 TGTGTAAAGCTACCTAAGAGACATGAGCCACGAGTATTAACCTCAGCCCTCTCTTG 1023
DB 164 TGTGTAAAGCTACCTAAGAGACATGAGCCACGAGTATTAACCTCAGCTCTCTTG 105

QY 1024 AGCCGTGACAGTGTGTATGTTAAAGTCCATGAGTGTGATGATCATGATG-ATTA 1082
DB 104 ACTTGTGAGAAACAGATATTTACACCCAGTGGAGATGTTAGACTCATGCTGTTA 45

QY 1083 CACAACGGTTTACAAATTTGTAATGATT 1111
DB 44 CACAATGGTTTAAANNNTTNTCTAAGNAGT 16

RESULT 7
LOCUS A0417854 575 bp DNA linear GSS 23-MAR-1999
DEFINITION RPCI-11-185M9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185M9,
DNA sequence.
ACCESSION A0417854
VERSION A0417854.1 GI:4475697
KEYWORDS GSS.

SOURCE human.
ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.

TITLE Use of BAC end sequences from library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: RPCI-11-185M9.TV
Contact: Shaying Zhao, William Nierman, Mark Adams

RESULT 9
A0827168/c 529 bp DNA linear GSS 27-AUG-1999
LOCUS HS_5256_B2_G09_T7A_RPCT-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate-832 Col-18 Row-N, DNA sequence.
ACCESSION A0827168
VERSION A0827168.1 GI:5793230
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 529)
Mallatras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mallatras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pletier de Jong
(pletier@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering-bac.htm>)
or from Research Genetics (<http://www.hscg.washington.edu>)
<http://www.hscg.washington.edu>
Plate: 832 row: N column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 529.
Location/Qualifiers
1..529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-832 Col-18 Row-N"
/clone_lib="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site:1: EcoRI; Site:2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
BASE COUNT 147 a 121 c 102 g 153 t 6 others
ORIGIN
Query Match 14.0%; Score 228.4; DB 12; Length 529;
Best Local Similarity 72.7%; Pred. No. 1.1e-37;
Matches 336; Conservative 0; Mismatches 115; Indels 11; Gaps 3;
OY 676 AATGCCAAGTTCATCACTGATGAAGAGGAGCAGAAAACGTGGCGGCAATT 735
|||||
DB 467 AATTCGCAAGTTCATCACTGATGAAGAGGAGCAGCAAGATGATGTCAGGCAATT 408
OY 736 CTGAATTCACCTTTATTCATAAATGTTGGGCGATTTTCAAGCTCCGACCTGGTGAAG 795
|||||
DB 407 CTGAATTCACCTTTATTCATAAAGCGTGGTGCATTTTGAAGTTACGGCTGGAGAGG 348
OY 796 AATATGACATTCAGGTGCAACCTTCCCTGCTGGATCCGATCAGATCAGCATCT 855
|||||
DB 347 AATATGACATTCAGGTGCAACCTTCCCTGCTGGATCCGATCAGATCAGCATCT 288
OY 856 TTGGGGCTTTCAAGTTGAGACATAGACATCTTTTCGTGGAACATTAGCATGGA 915
|||||

DB 287 TTGGGGCTTTAAAGTTGAGATATAGATTGAGCCCGCATTTTGGACTGT---ATGTA 231
OY 916 TGTCTAGATGTTTGAAGACCTTTCTTAAAA-----ATGATGATGCTATACATGCT 968
|||||
DB 230 TGTCTGATGTTTGGAAACATTTTTTAAACAGCCAGAAAGATGATATAGTGTGCT 171
OY 969 AAGACTAAGAGACATGGCCACGCGTATGAAGATCAGACGCTCTCTTGAGCCT 1028
|||||
DB 170 GAGACTAAGAGACATGGCCCGCAACGCTACAGCATCAGATCAGATCAGTCTTGACTT 111
OY 1029 GTACAGTGTGATATGATTAAGTCCATAGTGTATGATTCATGCTG-ATTACACA 1087
|||||
DB 110 GTAGAGAACACGAGATTTTACAGCCAGTGGAGATGATGATGCTGTTGATACAA 51
OY 1088 CGGTTTACATTTTGTATGATGTTTCTCTAAGATGACACAGA 1129
|||||
DB 50 TGTCTTGTAGATTGTTGTAAGAGTACTAAGCATGTCACACAA 9
RESULT 10
AG107545 659 bp. DNA linear GSS 03-NOV-2001
LOCUS AG107545
DEFINITION Pan troglodytes DNA, clone: PTB-112609.F, genomic survey sequence.
ACCESSION AG107545
VERSION AG107545.1 GI:16728063
KEYWORDS GSS; GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC library clone:PTB-112609.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (sites)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tokoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 659)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Tokoki,Y., Watanabe,H. and Sakaki,Y.
AUTHORS Direct Submission
TITLE Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC):
1-7-22 Suehiro-Chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbases@sc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..659
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-112609.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 181 a 168 c 121 g 189 t
ORIGIN
Query Match 12.6%; Score 205.4; DB 12; Length 659;
Best Local Similarity 86.3%; Pred. No. 7.7e-33;
Matches 227; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
OY 455 CATCCATCGGGTTCCCATTAAGTACACCTGCTCCCTGGTACACAGATGACGCTGGGC 514
|||||
DB 396 CTCTCCACAGGTTCCCATTAAGTGAAGTGTCTCTCTGGTACATGATCGGGGTGGGC 455

Qy	515	CAGATGTCCTAAACATGACGCTTAAGCAACGGAAACATTAAGGGTTTAAACCAAGTGGCTTTA	574
Db	456	CAGATGTCCTCAACATGACGCTTTTAAAGCAATGGAAACCTAATAGTTAATCAGATGGCTTTTA	515
Qy	575	TTACCTGTACGCCAACATTTGGCTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGA	634
Db	516	TTACCTGTATGCGAACATTTGGCTTTCGCATCATGAACCTCAGAGACCTAGCTACAGA	575
Qy	635	CTATCTCAGCTGATGCTGTATGTGTTAAAAACGACATCAAAATCCCAAGTTCCTCAATA	694
Db	576	ATATCTTCAACACTAAAGGTGTACGTACTCACTAAAAACGACATCAAAATCCCAAGTTCCTATAC	635
Qy	695	CCTGATGAAGGAGGAGGACAGA	717
Db	636	CCTGATGAAGGAGGAGGACACCA	658

Query Match	11.8%;	Score 192;	DB 9;	Length 419;
Best Local Similarity	73.3%;	Pred. No. 4.7e-30;		
Matches 321;	Conservative	0;	Mismatches 95;	Indels 22;
			Gaps	5;
QY 1013	CCCTCTCTTGAGCCCTGTACAGGTGTGTATGTATGTAAAGTCCANAGGTGATGTAGATTC	1072		
Db				
Db 4	CCATGCTCTTGACCTTTTGTATAGAACACACGCGATTTTACAGCCAGTGGAGATGTAGACTC	63		
QY 1073	ATGGTGATTTACACACGCTTTTACAAATTTGTATATGATTTCTTGAATTTGAACCAAGATTG	1132		
Db				
Db 64	ATGGTGATTTACAAATGTGTTTTTAAATTTTGTATATGAAATTCCTGAATTTAAACCAAGATTG	123		
QY 1133	GGAGAGTATTCGAGTCTTATGTAAAAACTTACACGAGCTATAGAAAGGGGTACAGT	1192		
Db 124	GAGCAATTTACGGGTTTGACCTTATGAGAAACGCAATGGTGGTAAAGGAGGGG-----	175		
QY 1193	CTCTGGGTCTAACCCCGAGCATGTGCACATGAGAAACCTTAAATTTAAGAGATGCCATG	1252		
Db 176	-----TTGGTCCTCTGGTCTATGTGCCCTTCGACAG-TCGAATGGAGAGGTGATC	226		
QY 1253	TCATTTGCAAAAGAAATGATAGTGTGAAGGGTTAACTTCTTTGAAATGTTACATGGCGTG	1312		
Db 227	T-ACGCAATTTGAAGGATCATCTGAAAGGGGCAAAATTCCTTTTGAATTTGTACATATGCTG	285		
QY 1313	GGACCTGCAATTAAGTCTTTTTTCTTATAGAGGAGAGAAAAATATATATATTTTATAT	1372		
Db 286	GAACTGTGAAAAA---TACTTTTCTTATATAGAGAG-AAAATATATGATTTTTTATAT	341		
QY 1373	AATGTCTTAAAGTTATTTTACAGTGTAAATGTTTCTGTGCAAGTTTGTAAATTAATTT	1432		
Db 342	AATATCTAAAGTTATTTTACAGATGTATATGTTTCTTGTGCAAGATTAATGTAAATTAATTT	401		
QY 1433	TGTGCTATATGATTTGAT	1450		
Db 402	TGTGCTATATGATTTGAT	419		

BASE COUNT	121 a	58 c	96 g	144 t
ORIGIN				


```
/dev_stage="Adult"  
/lab_host="SOLR"  
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:  
XhoI"  
BASE COUNT      102 a      80 c      78 g      100 t      2 others  
ORIGIN
```

```
Query Match      11.1%; Score 181.2; DB 9; Length 362;  
Best Local Similarity 71.3%; Pred. No. 8.4e-28;  
Matches 296; Conservative 0; Mismatches 59; Indels 60; Gaps 2;
```

```
QY 131 CGCTCTGTTCTGTTACTTTTGAGGCGAGATGATCTTACAGATAATCAGACAGACAC 190  
Db 1 CGCCCTGTTCTTCTTATTTTCAAGCGCGAGATGATCTTAAATATATTCAGACATGCGAC 60  
QY 191 TCACCTGTTTATATGATCTGAGACTCCATCGAATGAAAGCGAGATTTGAGAGCTCGACTCT 250  
Db 61 TCACCTGATTTATATGATTTTGAAGACTCCATGAAATGCAAGATTTTCAAGACACACTCT 120  
QY 251 CGAGAGTGAAGACAC-----ACTACCTGACTCTGTCAGAGAGATGAAACAGCCCTTTCA 304  
Db 121 GGAGAGTCAAGATATCAAAATTAATACCTGATTCATGAGAGATTAACAGAGCCCTTTCA 180  
QY 305 GGGGGCGGTGCAGAGAACTGCAACACATTTGTGGGCCACAGCGCTTCTCAGAGACTCC 364  
Db 181 AGGAGCTGTGCT----- 191  
QY 365 AGCTATGATGAGAGCGTCAATGTTGGATGTGGCCCGAGCGCAAGCCCTGAGCCCGAC 424  
Db 192 -----TGGTGATGAGTCAATGTTAGATCTGGCCCAAGAGAGAGAGAGCTTGAAGCTCAG 246  
QY 425 ATTTGCACACCTTACCATCATCATGCTGCCAGCATCCCATGGGTTCCCATTAAGTCACTCT 484  
Db 247 TTTTGGTCAATCTCATATTAATGATGCCACGACATCCCATCTGGTCCCATTAAGTGAAGTCT 306  
QY 485 GTCTCTTGGTACACGATCGAGGCGTGGGCCAAGATCTCTATCATGAGCTTAAGC 539  
Db 307 GTCTCTTGGTACATGATCGGNGTTGGGCCAAGATCTCTCATGACTTTTAAAGC 361
```

```
RESULT 13  
A2834036 618 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0116G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0116G04 R, DNA sequence.  
ACCESSION A2834036  
VERSION A2834036.1 GI:13003944  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 618)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
'M., Rose,M., Rose,R., Stokes,R., Tingy,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)
```

```
JOURNAL COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177
```

```
Email: edunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0116 row: G column: 04  
Seq primer: CACACAGAAACAGCATATGACC  
Class: plasmid ends
```

```
FEATURES High quality sequence stop: 618.  
Location/Qualifiers  
1..618  
source
```

```
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC2M0116G04"  
/clone_11b="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g114732114bp/AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

```
BASE COUNT      160 a      163 c      130 g      165 t  
ORIGIN
```

```
Query Match      10.2%; Score 165.8; DB 12; Length 618;  
Best Local Similarity 96.0%; Pred. No. 1.5e-24;  
Matches 170; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 147 TTTGAGCGGAGATGATCTCTTACAGAAATTCAGAAAGACGACCTACTGCTTTATTAAGA 206  
Db 26 TTCCCTCTGTAGATGATCTTAAACAGATATTCAGAAAGACGACCTACTGCTTTATTAAGA 85  
QY 207 ATCTGAGACTCATGAAACGAGATTTGACGACTCGACTGTGAGAGTGAAGACACA 266  
Db 86 ATCTGAGACTCATGAAACGAGATTTGACGACTCGACTGTGAGAGTGAAGACACA 145  
QY 267 CTACCTGACTCTGCGAGAGATGAACAACGCTTTACGGGGCGCTGCAGAGGAA 323  
Db 146 CTACCTGACTCTGCGAGAGATGAACAACGCTTTACGGGGCGCTGCAGAGGAA 202
```

```
RESULT 14  
A0817650 413 bp DNA linear GSS 26-AUG-1999  
LOCUS HS_5265.B1.D03-SP6E RPT-11 Human Male BAC Library Homo sapiens  
DEFINITION genomic clone Plate=841 Col=5 Row=H, DNA sequence.  
ACCESSION A0817650  
VERSION A0817650.1 GI:5780043  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 413)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.
```

```
JOURNAL COMMENT Sequence-tagged connectors: A sequence approach to mapping and  
MEDLINE scanning the human genome  
PROC. NATL. ACAD. SCI. U. S. A. 96 (17), 9739-9744 (1999)  
CONTACT: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington
```

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end web server: http://www.htsc.washington.edu

Plate: 841 row: H column: 5
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source

1. 413

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Plate841 Col-5 Row-H"

/clone_lib="RPCI-11 Human Male BAC library"

/sex="male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 108 a 82 c 100 g 123 t
ORIGIN

Query Match 7 1%; Score 116; DB 12; Length 413;
Best Local Similarity 69.9%; Pred. No. 4e-14; Indels 4; Gaps 1;

Matches 172; Conservative 0; Mismatches 70; Indels 4; Gaps 1;

OY 733 ATCTGATTCACCTTTATTCATTAATGTTGGGGATTTTCAAGCTCCAGCTGGG 792

DB 3 ATTCTAATTCATTTTATTCATTAACGTTGGCGATTTTAAAGTATGCTGGAG 62

OY 793 AAGAAATTAAGCATGAGTTCACACCTTCCTGCTGATCCGATCAAGTGCAGCT 852

DB 63 AGGAATTCATCATGAGGCTCCACCCCTCTACTGATCCGATCAAGTGCAGCT 122

OY 853 ACTTTGGGCTTCAAGTTCAGACATAGACTGATCATTTCTGGAACATTAGCAT 912

DB 123 ACTTTGGGCTTCTTAAGACGAGATATGATGGGCCACACTTTTGGAA---TGGAA 178

OY 913 GATATGCTAGATGTTGAACCTCTTAATAAATGATATGCTATATCATGTGAAG 972

DB 179 TGTATTCCTGATTTGGAACATTTTAAACAGCCAGCTAGATGTTATATGTGTGA 238

OY 973 CTACTA 978

DB 239 CTACTA 244

RESULT 15
BG203357/c 276 bp mRNA linear EST 21-APR-2001
LOCUS BG203357
DEFINITION RST22738 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG203357
VERSION BG203357.1 GI:13725044
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
Harrington, J. J., Sherif, B., Rundlett, S., Jackson, P. D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
'E., Veloso, N., Kliska, A., Hess, J., Colhen, K., Lo, K., Offenbacher,
'J., Danzig, J., and Ducar, M.
Creation of genome-wide protein expression libraries using random

JOURNAL
MEDLINE
21227151
COMMENT
Contact: Scott J. Cain
Atherys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atherys.com

activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
High quality sequence stop: 276.
Location/Qualifiers

FEATURES

source

1. 276

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Atherys RAGE Library"

/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', the Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 92 a 51 c 59 g 74 t
ORIGIN

Query Match 4.4%; Score 72.2; DB 10; Length 276;
Best Local Similarity 78.9%; Pred. No. 5.7e-05;

Matches 86; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 359 AGCTCCAGCTATGATGAGGAGGCTGATGTTGGCCAGCAGGAGCTGAGGC 418

DB 114 ATCTCCAGCGATGCTGATGCTGATGATCTGCGAAGAGGCAAGCTTGAAGC 55

OY 419 CCAGCAATTTGCACACCTCACCATCATGCTGCGCAGATCCCATCGGGT 467

DB 54 TCAGCTTTGCTCATCTCACTATTAAATGCCACCGACATCCATCTGCT 6

Search completed: July 8, 2002, 22:30:54
Job time: 8768 sec

THIS PAGE BLANK (USPTO)

PT develop products for augmenting an immune response for inhibiting and
 XX inflammatory response and for protection of cells
 PS Claim 27; Pages 55-57; 80pp; English.

Claim 27; Pages 55-57; 80pp; English.

This represents a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF- κ B)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF- κ B, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF- α . The products can also be used for detection and drug screening.

sq Sequence 294 AA;

Query Match	100.0%	Score 1561	DB 19	Length 294
Best Local Similarity	100.0%	Pred. No. 2	4e-140	
Matches 294	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	GVPHGSLHPAPSA	PAPAPPPAARSME	LLGLGLGOWC	STALFYFPAQMDPN	ISE	60	
Db	1	gvphgslhpapsap	pappppaarsmfl	llglglgwwc	stalfyfraqmdpn	ise	60	
QY	61	DSTHCFYKILILH	NADLQDSTLE	SEDTLPDSCR	RMKQAFQAGV	QKELHTVGPQ	RFSGA	120
Db	61	dsthcfyilrlh	nadlqdstlesed	tlpsccrmmqaf	gagvqkelh	ivgprfrsga		120
QY	121	PAMHGSMLDVAQ	KRPPAOPFALIT	INAASIPESG	SKVLLSSWYH	DHRGAKI	SNMPLSN	180
Db	121	pamhgsmlvaq	krppaopfalit	naasipsgskv	llsswyhnr	gakisnmplsn		180
QY	181	GKLRVNOQGFYU	LIANICERHHEH	SGSVPTDYLQ	LMLYVVKTS	IKIPSSHN	LKMGSGTKN	240
Db	181	gklrvngdgyu	lanicetfhhe	sgsvptcdyl	qmlmyvvtks	ikipsnlnk	mgsgtkn	240
QY	241	WSGNSEFFPYS	LNNGGFFKLAGE	ISIQVSNP	SLEDPDQATY	FEAGF	AKYQDDI	294
Db	241	wsgnseffysln	nggffklageeis	qvsnpstl	dpddqatyr	fgagfak	yqddi	294

RESULT	2
RAW60303	

ID	AAW68292	standard; protein; 294 AA

AC AAW68292;

DT 08-OCT-1998 (first entry)

DE NF- κ B receptor activator RANK ligand (RANKL).

RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; KW

KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

OS Mus musculus.

PN WO9828424-A2.

02-JUL-1998.

PD 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.
PF

PR 14-OCT-1997; 97US-0064671.

PR 07-MAR-1997; 97US-0813509.

PA (IMMV) IMMUNEX CORP.

(IMMV) IMMUNEX CORP.

PI Anderson DM, Galibert LJ, Maraskovsky E,

DR WPI; 1998-377655/32.

XX

PT New isolated receptor activator of necrosis factor- κ B - useful for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis

PS Example 7; Pages 55-57; 80pp; English.

This represents a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF- κ B)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF- κ B, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.

Sequence 294 AA:

Query Match	100.0%	Score 1561	DB 19	Length 294
Best Local Similarity	100.0%	Pred. No. 2.4e+140		
Matches 294	Conservative 0	Mismatches 0	Indels 0	Gaps 0

[illegible]

RESULT

ID AAE08737 standard; Protein; 294 AA

AC AAE08737;

DT 15-NOV-2001 (first entry)

DE Murine receptor activator of NF kappaB ligand (RANKL) protein.

XX	Murine: receptor activator of nuclear factor kappaB ligand; RANKL; NF-
KW	tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
KW	immune response; inflammatory response; graft-versus-host reaction;
KW	toxic shock; sepsis; acute inflammatory reaction; bone resorption;
XX	anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
OS	Mus musculus.
XX	
PN	US6271349-B1.
XX	
PD	07-AUG-2001.
XX	
PF	17-DEC-1998; 98US-0215649.
XX	
PR	23-DEC-1996; 96US-0059978.
PR	07-MAR-1997; 97US-0077181.
PR	14-OCT-1997; 97US-0064671.
PR	23-DEC-1996; 96US-0772330.
PR	07-MAR-1997; 97US-0813509.
PR	22-DEC-1997; 97US-0996139.
PA	
PA	(IMNV) IMMUNEX CORP.
P1	
P1	Dougal WC, Galburt L;
XX	
DR	WPI: 2001-520313/57.
DR	N-PSDB: AAD15310.
XX	
PT	New receptor activator of NF-kappaB (RANK) polypeptides, useful for
PT	regulating immune response, in screening for RANK inhibitors, or as an
PT	adjuvant therapy for disease characterized by neoplastic cells that
XX	express RANK -
PS	
PS	Example 15; Column 65-68; 47pp; English.
XX	
CC	The patent discloses novel receptor activator of nuclear factor (NF)-
CC	kappa (RANK) proteins and their corresponding DNAs. RANK is a member
CC	of the tumour necrosis factor (TNF) receptor superfamily and associates
CC	with TNF receptor associated factor (TRAF) 2 and 3 which are important
CC	in the regulation of immune and inflammatory response. The receptors
CC	are useful for regulating immune response and in screening for inhibitors
CC	of these receptors. The cytoplasmic domain of RANK is used in developing
CC	assays for inhibitors of signal transduction, e.g. for screening the
CC	molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
CC	TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
CC	are useful in ameliorating the negative effects of an inflammatory
CC	response that result from triggering of RANK, e.g. in treating toxic
CC	shock or sepsis, graft-versus-host reactions, acute inflammatory
CC	reactions and the effects of bone resorption. RANK acts as an anti-
CC	apoptotic signal and rescue the cells that express RANK from apoptosis.
CC	Soluble forms of the receptor are used in vivo or in vitro based
CC	screening tests for agonists or antagonists of RANK activity, as
CC	antagonists of RANK-mediated NF-kappa B activation, or to inhibit
CC	transduction of a signal via RANK. RANK compositions are used in the
CC	development of both agonistic and antagonistic antibodies, or as an
CC	adjuvant therapy for disease characterised by neoplastic cells that
CC	express RANK. Compounds that interfere with RANK/TRAF6 interactions
CC	are useful for modulating the formation of osteoclasts from osteoclast
CC	precursors and for modulating osteoclast function and activities. They
CC	are used as inhibitors of diseases associated with excess bone resorption
CC	and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
CC	useful for the expression of recombinant proteins, as probes for analysis
CC	of the presence or distribution of RANK transcripts, while the proteins
CC	are useful in preparing kits for the detection of soluble RANK, or
CC	monitor RANK-related activity. The present sequence is RANK ligand
CC	(RANKL) protein from murine.
XX	
XX	
SQ	Sequence 294 AA:
Query Match	100.0%; Score 1561; DB 22; Length 294;
Best Local Similarity	100.0%; Pred. No. 2,4e-140;

	Matches	294	Conservative	0	Mismatches	0	Indels	0	Gaps	0
OY	1	GVPHEGRILRPASAPARPPRAASMTLALLGLGQVCSIALFLYFRADMNRRISE	60							
Dd	1	gvphegrilrhpasaparpappraasmfllalglqgvcsiafllyfrqmdpnrlise	60							
OY	61	DSTHCFYRILRLHENADLDOSTIESEDPLPDSCRYMKAKAFQAVOKELQHTIYGPRFSGA	120							
Dd	61	dsthcfyllrltlhenadldqdstlesedclpdscrrmkafqgaavokelqlhyvgprffsga	120							
OY	121	PAMMGSLMDVAOQRKPEAOFPAILTTINASTIPSGSHKVTLUSSWYHDRGMAKISMNLTISN	180							
Dd	121	pammegswladvagrkpeaqpfahltlnaaasipgsghkvltisswyhdrgakismnltisn	180							
OY	181	GLRLYNODGFYYLYANICFRHNHTSGSVPTDTLOIMVVVVTSIKTIPSSHNLMMKGSRKN	240							
Dd	181	glrlryndgfyylyanlcfrhnetsgsvptcdtqlmvyvvvtstiklpsshnlmmkgstrkn	240							
OY	241	WSGNSEFHFTYSINVGGFFKLRRAGEEISIQVSNPSSLDDPDQATVGARKVDID	294							
Dd	241	wsgnesehfhtysinvggffklrrageeisiqvsnpslldpdqatylfgarkvqidid	294							
	RESULT	4								
	AAE04425									
	AAE04425	standard; Protein: 294 AA.								
	AAE04425:									
	04-SEP-2001	(first entry)								
	XX									
	DE	Murine receptor activator of NF-chi B ligand (RANKL) protein.								
	XX									
	KM	Murine: receptor activator of NF-chi B; RANK: tumour necrosis factor;								
	KW	CD40: TNF receptor-associated factor; TRAF: ligand; immune response; TNF;								
	KM	chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.								
	OS	Mus musculus.								
	XX									
	FT	Key Location/Qualifiers								
	FT	Region 139..294								
	FT	/note="Receptor binding region"								
	PN	US6242213-B1.								
	XX									
	PD	05-JUN-2001.								
	XX									
	PF	22-DEC-1997; 97US-0995659.								
	XX									
	PR	23-DEC-1996; 96US-0059978.								
	PR	07-MAR-1997; 97US-0077181.								
	PR	14-OCT-1997; 97US-0064671.								
	XX									
	PA	(IMMV) IMMUNE CORP.								
	XX									
	PI	Anderson DM;								
	XX									
	DR	WPJ: 2001-407216/43.								
	DR	N-PSTD: AAD08714.								
	PT	New DNA molecules, useful for producing ligands (which are useful for								
	PT	regulating immune response and in screening for inhibitors of NF-chi B								
	PS	receptor activator) of the receptor activator of NF-chi B (RANK)								
	XX									
	XX	Example 7; Column 59-62; 43pp; English.								
	CC	The present invention relates to receptor activator of NF-chi B (RANK)								
	CC	DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to								
	CC	chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane								
	CC	proteins respectively. RANK is a member of the tumour necrosis factor								
	CC	(TNF) superfamily and it closely resembles CD40 in the extracellular								
	CC	region. RANK associates with TNF receptor-associated factor (TRAF) 2								
	CC	and TRAF3. The DNA molecules are useful for producing ligands of RANK,								

CC The ligands are useful for regulating immune response and in screening
XX for inhibitors of RANK. The present sequence is murine RANKL protein.
50 Sequence 294 AA;

SQ Sequence 294 AA;

Query Match	100.0%	Score 1561;	DB 22;	Length 294;
Best Local Similarity	100.0%	Pred. No. 2,4e-140;		
Matches 294; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	GVHEGGLHPAPSA	PAPRPPAARSMEFLALGIGLOVCSIALFLYFAQNDPNRISE	60
Qy	1	GVHEGGLHPAPSA	PAPRPPAARSMEFLALGIGLOVCSIALFLYFAQNDPNRISE	60
Db	1	gvnhegrlhpapsapappppaasrsmflalglgigvcsialflyfraqndpnri	se	60
Qy	61	DSTHCFYRILILHFNADLODSTLESEDTLPDSCRMMQAFQAGVQKELHITVBPQRFSGA	1200	
Db	61	dsthcfyrlilrhenadlqdstlesedtlpdsctrmmqafgagvqkelhitypqrfsq	1200	
Qy	121	PAMEGSMULDVAQGRKPRAPFPALITINAAISIPSGSHKVTLLSMYHNRGAKITSMNTLSN	1800	
Db	121	pamegswldvayqgrkprapfialltnaaipsghskvtllssmyhnrqakitsmnlsm	1800	
Qy	181	GKLRYNOGFYUVAANICFRHHEHNSGVPTDYLOLAMYVVKTSIKRIPSSNNLMKGSTKN	2400	
Db	181	gklyrnoqgfyllyanlcfrhhecsgrptdyldlmyvvtksikrpsnnlmkgsctkn	2400	
Qy	241	WSGNESEFPFYSINVGFFKLRAEBEISTQVSNPSBLDPDDDATYFGAFKXQDID	294	
Db	241	wsgneeflfsynvgffklrangelstqysnpsblpddqatcyfgafkxqddid	294	

RESULT	5
AAE01992	
ID	AAE01992 standard; Protein; 294 AA.

AC AAE01992;

DT 31-JUL-2001 (first entry)

DE Murine RANKL (receptor activator of NF-kappaB ligand) protein.

AK Mouse; receptor activator of NF- κ Bpab; RANK; nuclear factor- κ Bpab;
 KM NF- κ Bpab; tumour necrosis factor; TNF; type I transmembrane protein;
 KM TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopontin;
 KM inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KM immune system dysfunction; familial expansile osteolysis; FEO;
 KM early onset Paget's disease of bone; EP; cytostatic.

Musculus.

PN WO200136637-A1.

PD 25-MAY-2001.

PF 14-NOV-2000; 2000WO-US31459.

PR 17-NOV-1999; 99US-0442029.

PA (IMMV) IMMUNEX CORP

PI Anderson DM, Hughes AE;

DR WPI; 2001-329222/34.

XX

XX New DNA encoding a receptor activator of NF-kappaB polypeptide for the treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
PT
PS Disclosure; Page 74-75; 96pp; English.

CC The present invention relates to a novel receptor, referred to as RANK
AA (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a Type I

transmembrane protein that interacts with TNF receptor-associated factors (TRAFs). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNMs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct gene-activating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The protein amino acid sequence is murine RANKL (muRANKL) protein.

SQ Sequence 294 AA;

Query Match	100.0%	Score 1561;	DB 22;	Length 294;
Best Local Similarity	100.0%	Pred. No. 2,4e-140;		
Matches 294; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 GVHEGRLHPAPSA PAPPAPPAASRSMFLALLIGLGQWCVSTALLETYPRAOMDPNISE 60

Db 1 gvphegplhpapsapapapppaasrsmflalliglgqvcsaliflyfraqmprlse 60

QY 61 DSTHGFYRLRLHENADLQDSTLESEDTLPDCRRMKOAFGAQOKELQHTVGPQFSGA 120

Db 61 dsthgfyrllrlhenadlqdstleesetlpsccrrmkqafgavqkelqhlvpgqrtsa 120

QY 121 PAMFGSWLDVAQOKRPPAORPAHLTTAASTIPSGSHKVTLSMYHNRGAQKTSNMFLSN 180

Db 121 pammgswldvagrqrpeagrfahltnaasipsgshkvltssvyrhgwaktsnmflsn 180

QY 181 GKLRVNODFYYLYANICFRHHETSGSVPTDYLDLMYVVKTSIKIPSSINLMKGSTKN 240

Db 181 gklyrnqdgfylylanicfrhetsgsrptdyldlmyvvtksikipsnlnmkgstkn 240

QY 241 WSGNSEFHFYSINVGGEFKLRAGEISTQVNSPSTLDEDDDATYFGAKVQDID 294

Db 241 wsgnsefhfyslnvggikflrgeetsqvnpsltldpddqdaeyfgakvqddid 294

RESULT	6
AAW83194	
ID	AAW83194 standard; Protein; 316 AA

AAW83194; AC

DT 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the 32D-F3 ins.

Human: osteoprotegerin binding protein; OPB binding protein; arthritis
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
 KW hypercalcaemia, osteoclast differentiation and activation receptor;
 KW Paget's disease.

OS Homo sapiens.

PN W09846751-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

PA (AMGE-) AMGEN INC


```

XX      Boyle WJ:
PI      WPI: 1998-594578/50.
XX      DR      N-PSDB: AAV70284.
XX      PT      Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT      e.g., treating bone diseases by modulating osteoclast differentiation
XX      and for diagnosis
XX      PS      Claim 19: Fig 1: 47pp: English.
XX
CC      The present sequence is human osteoprotegerin (OPG) binding protein.
CC      Host cells transfected with vectors containing nucleic acid molecules
CC      encoding OPG binding protein are used to produce recombinant OPG binding
CC      protein. OPG binding protein is used in binding assays to determine
CC      osteoprotegerin (OG) in biological samples; to screen for specific
CC      binding agents (particularly agonists and antagonists, including
CC      intracellular proteins); to raise Ab (useful in immunoassays for
CC      detection of OPG binding protein) and to identify compounds that
CC      modulate binding of OPG binding protein to osteoclast differentiation
CC      and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC      binding protein can be used to detect OPG binding protein-encoding
CC      sequences, e.g., screening for related sequences, also to produce
CC      transgenic animal models, while complementary sequences are used for
CC      antisense regulation of OPG binding protein expression. Modulators of
CC      OPG binding protein, particularly soluble forms of OPG binding protein
CC      or Ab, are used to treat or prevent bone diseases, e.g., osteoporosis,
CC      bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC      disease, periodontal disease, osteoporosis, loosening of prostheses,
CC      optionally in combination with agents that promote bone growth.
XX      Sequence 316 AA:
SQ
Query Match          99.6%: Score 1554; DB 19: Length 316;
Best Local Similarity 99.7%: Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 GVPHEGRLHAPAPAPAPAPAPASRSNMFLLGLGQVCSIALFLYFRAMDPNRISF 60
DB      23 gvphegrlhpapapapapapapasmflla1lg1gqvcsialfllyfragmdpnriise 82
OY      61 DSTHCFYRLRLHFNADLSDTLESDTLPSDCRRKQAFQAVQKELQIHVGPQRFSGA 120
DB      83 dsthcfyrlrlhfnadlstdtlesedtlpdsccrmkqafgavqkelqihvqpqrfsga 142
OY      121 PAMMEGSLDVAQRGRPEAPFAHLITINASTIPSGSHKVTLSWYHHRGNAKTSNMTLN 180
DB      143 pammegswldvagrgrpeapfahlitinaasipsgshkvltswyhrgrgnaaktsnmcln 202
OY      181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWVYVVKTSIKIPSSHNLMKGGSTKN 240
DB      203 gklrvngdgffyylyanicfrhhetsgsvpdyqlmwvyvvtksiklpsshnlmkggstkn 262
OY      241 WSGNSEFHYSINVGGFYKLRAGEEISIOVSNPSLLDPDDATYFGAFKVOODID 294
DB      263 wsgnsafhysinvggfyklrageeisiovsnpsslldpddatylfgafkvodid 316
RESULT 7
AAW83017
ID      AAW83017 standard; Protein: 316 AA.
AC      AAW83017;
XX      10-FEB-1999 (first entry)
XX      Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
DE      Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW      osteoclast; bone absorption factor; bone disorder; calcium metabolism.
XX

```

```

OS      Unidentified.
XX      PN      WO9846644-A1.
XX      PD      22-OCT-1998.
XX      PF      15-APR-1998; 98WO-JP01728.
XX      PR      02-DEC-1997; 97JP-0332241.
XX      PR      15-APR-1997; 97JP-0097808.
XX      PR      09-JUN-1997; 97JP-0151434.
XX      PR      12-AUG-1997; 97JP-0217897.
XX      PR      21-AUG-1997; 97JP-0224803.
XX      PA      (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX      PI      Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI      Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI      Washida N, Yamaguchi K, Yano K, Yasuda H;
DR      WPI: 1998-594563/50.
XX      DR      N-PSDB: AAV69886.
XX      PT      Protein binding to osteoclastogenesis inhibitory factor - useful
PT      for, e.g., treatment and investigation of disorders of bone and
XX      calcium metabolism
XX      PS      Claim 8: Pages 106-108; 151pp; Japanese.
XX      CC      The present sequence represents an osteoclastogenesis inhibitory factor
CC      (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC      separation and maturation of osteoclasts in the presence of bone
CC      absorption factors such as calcitriol or parathyroid hormone (PTH).
CC      OBM is isolated from stroma cells cultured in the presence of a bone
CC      absorption factor by separation and solubilisation of membrane proteins
CC      then affinity chromatography using OCIF. It exists in a full-sequence
CC      form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC      used for screening potential inhibitors and modifiers of its biological
CC      activity, and screening for receptors to OBM which mediate its function.
CC      These substances can then be used in the treatment of disorders of bone
CC      function and calcium metabolism. The antibodies can be used for assay
CC      of the protein, for investigative and diagnostic purposes, and as
CC      components of drugs.
XX      Sequence 316 AA:
SQ
Query Match          99.6%: Score 1554; DB 19: Length 316;
Best Local Similarity 99.7%: Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 GVPHEGRLHAPAPAPAPAPAPASRSNMFLLGLGQVCSIALFLYFRAMDPNRISF 60
DB      23 gvphegrlhpapapapapapapasmflla1lg1gqvcsialfllyfragmdpnriise 82
OY      61 DSTHCFYRLRLHFNADLSDTLESDTLPSDCRRKQAFQAVQKELQIHVGPQRFSGA 120
DB      83 dsthcfyrlrlhfnadlstdtlesedtlpdsccrmkqafgavqkelqihvqpqrfsga 142
OY      121 PAMMEGSLDVAQRGRPEAPFAHLITINASTIPSGSHKVTLSWYHHRGNAKTSNMTLN 180
DB      143 pammegswldvagrgrpeapfahlitinaasipsgshkvltswyhrgrgnaaktsnmcln 202
OY      181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLMWVYVVKTSIKIPSSHNLMKGGSTKN 240
DB      203 gklrvngdgffyylyanicfrhhetsgsvpdyqlmwvyvvtksiklpsshnlmkggstkn 262
OY      241 WSGNSEFHYSINVGGFYKLRAGEEISIOVSNPSLLDPDDATYFGAFKVOODID 294
DB      263 wsgnsafhysinvggfyklrageeisiovsnpsslldpddatylfgafkvodid 316
RESULT 8

```

AAW59654
ID AAW59654 standard; Protein; 316 AA.
XX
AC AAW59654;
XX
DT 24-SEP-1998 (first entry)
XX
DE Amino acid sequence of mouse 499E9 protein.
XX
XX Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW acute inflammatory response; antibody; antigen; cancer.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT 1..49
FT Domain /note="intracellular domain"
FT 70..316
FT Domain /note="extracellular domain"
XX
PN WO9825958-A2.
XX
PD 18-JUN-1998.
XX
PE 12-DEC-1997; 97WO-US22766.
XX
PR 13-DEC-1996; 96US-0032846.
XX
XX (SCHE) SCHERING CORP.
XX
PI Gorman DM, Mattson JD;
XX
XX WPI; 1998-348452/30.
DR N-PSDB; AAV41489.
XX
PT Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX associated with abnormal physiology or development
XX
PS Claim 1; Pages 8-11; 59pp; English.
XX
XX This is the amino acid sequence of the mouse 499E9 protein, used
CC in the method of the invention to treat conditions associated with
CC abnormal physiology or development. The 499E9 protein is expressed
CC highly on polarised Th1 T cells, binding of 499E9 to its receptor may
CC result in either immune cell expansion or apoptosis. Antagonists of
CC 499E9 may be used to modulate immune responses in abnormal situations,
CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
CC acute inflammatory responses in which T-cell expansion, activation or
CC immunological T-cell memory play an important role. The antibodies
CC can be used to raise anti-idiotypic antibodies which will be useful
CC in detecting or diagnosing various immunological conditions related to
CC the expression of antigens of 499E9. The antibodies, and fragments of
CC 499E9 can be used in the treatment of conditions associated with
CC abnormal physiology or development, including abnormal proliferation
CC (e.g. cancerous conditions) or degenerative conditions.
XX
SQ Sequence 316 AA;
Query Match 99.6%; Score 1554; DB 19; Length 316;
Best Local Similarity 99.7%; Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGPIHPAPAPAPAPAPASRSKFLALIGLGOVCSIALFLFRQMDPNRISE 60
DB 23 gvphegphlpapapapapapapasmfiallgigvcsialflfrqmdpnriise 82
QY 61 DSTHCFYILIRHFNADLSDSEDLPLPSGCRMKOAFQAVOKELOHIVGPREFGA 120
DB 83 dsthcfyilirhfnadlsgdesdlplpsgcrmkqatfgavqkqlhivgprfsga 142

QY 121 PAMMEGSMILDVAORGKPEAFHLLTINAASIPSGSHKYTLSSWYHGRWAKISNNTLSN 180
DB 143 pammegswildvaorgkpeagpfhlhlnaasipsgshkvtlsswydrgwakismntlsn 202
QY 181 GKLRVNDGFRYYLIYANICFRHHETSGSVPTDYQLMAYVYVVKTSIKRIPSSHNLMMKGSTKN 240
DB 203 gklrvndgfylyianicfrhethetsgsvptdyqlmavyvvtksikrpsshnlmkgstkn 262
QY 241 WSGNSEHFYSINWGFPEKLRAGEEISIOVSNPSLDDPDODATYFGAFKVDID 294
DB 263 wsgnsehfysinwgfpeklrageeisiovsnpsslddpodatyfgafkvqdid 316

RESULT 9
AAV17874
ID AAV17874 standard; Protein; 316 AA.
XX
AC AAV17874;
XX
DT 17-AUG-1999 (first entry)
XX
DE Murine TRANCE.
XX
XX TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
KW TNF-related activation induced cytokine; immune response; cancer;
KW autoimmune disease; HIV; hypersensitivity; allergen.
XX
OS Mus musculus.
XX
PN WO9929865-A2.
XX
PD 17-JUN-1999.
XX
PE 14-DEC-1998; 98WO-US26486.
XX
PR 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1998; 98US-0034099.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Choi Y, Josien R, Steinman R, Won B;
PI
XX
XX WPI; 1999-385609/32.
DR N-PSDB; AAX80224.
XX
XX TNF like proteins for treating autoimmunity and cancer
XX
PS Claim 9; Fig 3; 164pp; English.
XX
XX The present sequence represents murine TNF-related activation induced
CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
CC variants, fragments, derivatives or analogues may be used as modulators
CC of immune response in a mammal comprising, antisense sequences to
CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
CC Agonists and antagonists of TRANCE, can be used to modulate immune
CC response by increasing or decreasing the life span of mature dendritic
CC cells and increasing or decreasing T cell activation. These techniques
CC are especially useful for treating immune system related conditions such
CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
CC The TRANCE polypeptides can be used to increase the viability of
CC dendritic cells in vivo or in vitro, especially when used in conjunction
CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
CC CD40L or TNF-alpha).
XX
SQ Sequence 316 AA;
Query Match 99.6%; Score 1554; DB 20; Length 316;
Best Local Similarity 99.7%; Pred. No. 1.2e-139;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Tue Jul 9 13:21:00 2002

us-09-865-363-11.rag

Page 11

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)


```

Query Match 100.0% Score 1561: DB 3: Length 294:
Best Local Similarity 100.0% Pred. No. 2 8e-153:
Matches 294: Conservative 0: Mismatches 0: Indels 0: Gaps
0Y 1 GVPHEGFLHAPASAPAPPPAPASBSMFLALLGGLGVVCSIALFLYFRAQMDPNRISE 600
DB 1 GVPHEGFLHAPASAPAPPPAPASBSMFLALLGGLGVVCSIALFLYFRAQMDPNRISE 600
0Y 61 DSTHCFRILRLHENDLDDSTLSEEDTLPOSCRMMQAFQGANVOKELOHVGPQRSGA 12
DB 61 DSTHCFRILRLHENDLDDSTLSEEDTLPOSCRMMQAFQGANVOKELOHVGPQRSGA 12
0Y 121 PAMMEGSMILVAORGPKEAPFAHLITINAASIPSGSHKVTLSWYHDRGAKISNMTLN 18
DB 121 PAMMEGSMILVAORGPKEAPFAHLITINAASIPSGSHKVTLSWYHDRGAKISNMTLN 18
0Y 181 GKLRVNDGFFVLLYANICERHHTSGSVPTDYLQMLVYVKTISIKIPSSHNLMKGSTKN 24
DB 181 GKLRVNDGFFVLLYANICERHHTSGSVPTDYLQMLVYVKTISIKIPSSHNLMKGSTKN 24
0Y 241 WSGSSEHFHSIVGGEFFRLAGEETISIOVNSPLDDPDQATYFGAFKVOIDD 294
DB 241 WSGSSEHFHSIVGGEFFRLAGEETISIOVNSPLDDPDQATYFGAFKVOIDD 294

RESULT 2
US-08-995-659-11
: Sequence 11, Application US/08995659
: Patent No. 6242213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-11

```

[illegible]

3 RESULT
US-09-215-649A-11
: Sequence 11, Application US/09215649A
: Patent No. 6271349
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Masakovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/215,649A
: FILING DATE: 17-Dec-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/996,139
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US98 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: US98 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
:

SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 100.0%; Score 1561; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 2,8e-153;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGAGVCSIALFLYFRAMPNRISE 60
DB 1 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGAGVCSIALFLYFRAMPNRISE 60
QY 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMKQAFQAVOKELQHVGPORFSGA 120
DB 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMKQAFQAVOKELQHVGPORFSGA 120
QY 121 PAMMEGSLDVAQGRKPEAPFAHLITNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
DB 121 PAMMEGSLDVAQGRKPEAPFAHLITNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
QY 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
DB 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
QY 241 WSGNSEHFYSINVGGFEKFLRAGEEISTQVSNPSILDDPDODATYFGAFKVDID 294
DB 241 WSGNSEHFYSINVGGFEKFLRAGEEISTQVSNPSILDDPDODATYFGAFKVDID 294

RESULT 4
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: BOYLE, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-842-7

Query Match 99.6%; Score 1554; DB 2; Length 316;
Best Local Similarity 99.7%; Pred. No. 1,7e-152;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGAGVCSIALFLYFRAMPNRISE 60
DB 23 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGAGVCSIALFLYFRAMPNRISE 82
QY 61 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMKQAFQAVOKELQHVGPORFSGA 120
DB 83 DSTHCFYRLRLHENADLQDSTLSEEDTLPSDCRMKQAFQAVOKELQHVGPORFSGA 142
QY 121 PAMMEGSLDVAQGRKPEAPFAHLITNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 180
DB 143 PAMMEGSLDVAQGRKPEAPFAHLITNAASIPSGSHKVTLSWYHGRMAKISNMTLSN 202
QY 181 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 240
DB 203 GKLRVNDGFFYYLVANICFRHETSGSVPTDYQLMYYVVTSTIKIPSSHNLKMGSGSTKN 262
QY 241 WSGNSEHFYSINVGGFEKFLRAGEEISTQVSNPSILDDPDODATYFGAFKVDID 294
DB 263 WSGNSEHFYSINVGGFEKFLRAGEEISTQVSNPSILDDPDODATYFGAFKVDID 316

RESULT 5
US-08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-362-2

Query Match 99.6%; Score 1554; DB 4; Length 316;
Best Local Similarity 99.7%; Pred. No. 1,7e-152;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GVPHEGRLHAPASAPAPAPPAASRSMFLALLGLGAGVCSIALFLYFRAMPNRISE 60
|||||

```
Db 23 GVPHEGPLHPAPSAAPAPPPAPASRSMFLALLGLGLGVVCSIALFLYFRAMDPNRISE 82
QY 61 DSTHCFYRLRLRHENADLQDSTLESEDTLPDSCRMMKQAFQGA VQKELQHIIVGPORFSGA 120
Db 83 DSTHCFYRLRLRHENAGLQDSTLESEDTLPDSCRMMKQAFQGA VQKELQHIIVGPORFSGA 142
QY 121 PAMMEGSMWLDVAORGRKEAPQFAHLITINAASIPSGSHKVTLSWYHDRGNAKISNMTLN 180
Db 143 PAMMEGSMWLDVAORGRKEAPQFAHLITINAASIPSGSHKVTLSWYHDRGNAKISNMTLN 202
QY 181 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLQMWYVYKTSIKIPSSHNLKMGSGSTKN 240
Db 203 GKLRVNDGFFYYLYANICFRHHETSGSVPTDYQLQMWYVYKTSIKIPSSHNLKMGSGSTKN 262
QY 241 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDQDATYFGAFKQVODID 294
Db 263 WSGNSEFHFYSINVGFFFKLRAGEEISIOVSNPSLLDPDQDATYFGAFKQVODID 316

RESULT 6
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Biv
; CURRENT APPLICATION NUMBER: US/09/052, 521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880, 855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842, 842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRP
; ORGANISM: Mouse
US-09-052-521C-2

Query Match 99.6%; Score 1554; DB 4; Length 316;
Best Local Similarity 99.7%; Pred. No. 1.7e-15;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996, 139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/064, 671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/813, 509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/772, 330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

Query Match 85.0%; Score 1326.5; DB 3; Length 317;
Best Local Similarity 84.5%; Pred. No. 5.4e-129;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;
```

[illegible]

		85.0%;	Score 1326.5;	DG 4;	Length 317;	
	Query Match	Similarity	84.5%;	Pred. No. 5.4e-129;		
	Best Local	Similarity	84.5%;	Pred. No. 5.4e-129;		
	Matches	220;	Conservative	16;	Mismatches	17;
					Indels	3;
					Gaps	2;
QY	1	GVTHEGRLPRADSPARAPRPPAPRPAASRSMELALLGLGCVSIALFLTPYAPRADMPIRIS	60			
Db	23	GATHEERPLH-APPAPRAPHOPRPAASRSMELVALLGLGCVSIALFLTPYAPRADMPIRIS	81			
QY	61	DSTHCEYRLRLRHEMADLODSTLESSEDT--LPDSGRMKAKFGCAVOKELQHTVGGQRSS	118			
Db	82	DGTHCITRLRLRHEMADLODSTLESSEDTKLPLDSCRTKAKFGCAVOKELQHTVGGQHTLR	141			
QY	119	GAPAMEGSLDYAORGRKPAORFANHTLTINAASIPSSKHVTLSSWYHNRGMAKISNMTL	178			
Db	142	AEKAMWDGSMILARSKLEORFANHTLTINATDIPSSKHVTLSSWYHNRGMAKISNMTE	201			
QY	179	SNKTLVANDGFEYUULANICFRNHETSGSVPTDLOLAMYVVTSTIKIRSNHLMKGGST	238			
Db	202	SNKTLVANDGFEYUULANICFRNHETSGDLATLDTLOLAMYVVTSTIKIRSNHLMKGGST	261			

;; INFORMATION FOR SEQ ID NO: 2;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 281 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 16.6%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPDSCRMKQAFQGAOVK-----ELQHIYGPQRSGAPAM 124
DB 65 WDP--NDEESMNSPCWQVKQOLVRLKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 174
DB 114 -----VREGPQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLLANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHLRNGELVIEHKGFYIYSQTYFRQEEIKENTKNDKQMOVYIKYT--SYDPDILLK 224
OY 225 GSGTRKNSGSEFHFYSINVGFFKLAGEEISIOVSNPSLLDDPDODATYFGAKV 290
DB 225 SARNSCWSKDAEYGLISTYOGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFV 280

RESULT 13
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584, 031A
; CURRENT FILING DATE: 1996-01-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 16.6%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPDSCRMKQAFQGAOVK-----ELQHIYGPQRSGAPAM 124
DB 65 WDP--NDEESMNSPCWQVKQOLVRLKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 174
DB 114 -----VREGPQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLLANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHLRNGELVIEHKGFYIYSQTYFRQEEIKENTKNDKQMOVYIKYT--SYDPDILLK 224

OY 235 GSGTRKNSGSEFHFYSINVGFFKLAGEEISIOVSNPSLLDDPDODATYFGAKV 290
DB 225 SARNSCWSKDAEYGLISTYOGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFV 280

RESULT 14
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: APO-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-496-1

Query Match 16.6%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1,1e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

OY 21 PAASRMFLALGLGQVCSIALFLYFRAQMD--PNRISEDTHCFYRIILRHENADL 78
DB 10 PSLGQTCVLIVFTVLLQSLCAVAVTYVFTNELKQMDKYSKSGIACF-----LKEDDSY 64
OY 79 QDSTLESDTLPDSCRMKQAFQGAOVK-----ELQHIYGPQRSGAPAM 124
DB 65 WDP--NDEESMNSPCWQVKQOLVRLKMLRTSEETISTVOEKQONISPL----- 113
OY 125 EGSWLDVAQRKPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 174
DB 114 -----VREGPQRYA--AHITGRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
OY 175 NMTLSNGKLAVNODGFYLLANICFRHNETSGSVPTDYQLAMVYVVKTSIKIPSSHNLK 234
DB 166 NLHLRNGELVIEHKGFYIYSQTYFRQEEIKENTKNDKQMOVYIKYT--SYDPDILLK 224
OY 225 GSGTRKNSGSEFHFYSINVGFFKLAGEEISIOVSNPSLLDDPDODATYFGAKV 290
DB 225 SARNSCWSKDAEYGLISTYOGGIFELKENDRIEVSVTNEHLIDMDHEASFFGAFV 280

RESULT 15
US-08-883-086-10
; Sequence 10, Application US/08883086

QY	163	SWYHDGRCAKSNMPLTSLNGKRLVRNODGEYLYLVANTICFPHHETSGVPPDIQYQWLVYVYKT	222
QY	163	SWYHDGRCAKSNMPLTSLNGKRLVRNODGEYLYLVANTICFPHHETSGVPPDIQYQWLVYVYKT	222
DB	161	EMEDYTGIVTLISGVYKKKGGGLVINETGLYFYVSKRYEFGOSCN-----LPLSHKVMYR	214
QY	223	SIKIPSSHNLMKSGSTKMMWGSNEFHFYSINVGGEFKLRAGEISIOVNSDLDPDDA	282
DB	215	NSKYRQDLYVME-CRNMSTCTTGGMARSSYLGAVFNLTSDHLIVNSELVLNFEESQ	273
QY	283	TYEGAFV 230	
DB	274	TEFGGLYKL 281	
RESULT	5		
CD40 ligand	human		
N:Alternate names:	glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein		
C:Species:	Hom sapiens (man)		
C:Date:	02-Jul-1996 #sequence,revision 02-Jul-1996 #text,change 20-Apr-2001		
C:Accession:	S28017, JH0793; S26694; S28852; I53476; S25684; S30593		
R:Holtenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;			
EMBO J. 11, 4313-4321, 1992			
A:Title:	The human T cell antigen gp39, a member of the TNF gene family, is a ligand for		
A:Reference number:	S28017; MUID:93049181		
A:Accession:	S28017		
A:Molecule type:	mRNA		
A:Residues:	1-261 <GR>		
A:Cross-references:	EMBL:Z15017; NID:938483; PIDN:CA478737.1; PID:938484		
R:Spriggs, M.K.; Armistage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T			
J. Exp. Med. 176, 1543-1550, 1992			
A:Title:	Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin		
A:Reference number:	JH0793; MUID:93094757		
A:Accession:	JH0793		
A:Molecule type:	mRNA		
A:Residues:	1-261 <SP>		
A:Cross-references:	GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412		
A:Experimental source:	peripheral blood T-cell		
R:Grif, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroccek, R.A.			
Eur. J. Immunol. 22, 3191-3194, 1992			
A:Title:	Cloning of TRAP, a ligand for CD40 on human T cells.		
A:Reference number:	S26694; MUID:93076854		
A:Accession:	S26694		
A:Status:	Preliminary		
A:Molecule type:	mRNA		
A:Residues:	1-261 <GR>		
A:Cross-references:	EMBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270		
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Lile, P.; Jomotte, T.; Bonney, J.			
FEBS Lett. 315, 259-266, 1993			
A:Title:	Human CD40-ligand: molecular cloning, cellular distribution and regulation of e		
A:Reference number:	S28852; MUID:93138085		
A:Accession:	S28852		
A:Molecule type:	mRNA		
A:Residues:	1-261 <GAU>		
A:Cross-references:	EMBL:L07414; NID:9180123; PIDN:AAA35662.1; PID:9180124		
A:Note:	The sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln		
C:Genetics:			
A:Gene:	GDB:CD40LG; HIGM1; TMD3		
A:Cross-references:	GDB:120632; OMIM:308230		
A:Map position:	Xq26-Xq26		
C:Keywords:	glycoprotein; transmembrane protein		
F:13-44/Domain:	transmembrane #status predicted <TM>		
F:45-261/Domain:	extracellular #status predicted <EXT>		
F:6,240/Binding site:	carbohydrate (Asn) (covalent) #status predicted		
Query Match	10.9%; Score 169.5; DB 2; Length 261;		
Best Local Similarity	25.7%; Pred. No. 6,6e-07;		
Matches	75; Conservative 50; Mismatches 116; Indels 51; Gaps 16;		
QY	11	APSPAPAPAPAPASMPALALLGLGLGVCSIALF-LYFPAQMDPNRISDSTHCYRI 69	
DB	9	SPRSAAVGLP--ISKIKIMVLLTVLITOMIGSALFAVAVLHRRLD--KIEBER----- 57	

Oy	70	LRLHEADLDQSTLESDTLPDPS----	CRMKQAQGAVOKELOHIVGPRQRSGAPAMM	124
		: : : : :	-----LNKREBTK	107
Dd	58	-NLHEFEVEM-KTIOCRNCTGRSLILNC	EELISQDFEGEV-KDIM-----	
Oy	125	EGSMULDVAORGPPEAOPFAHLITINAS	IPSGSHKYVLSSMYHDRCAGAKISN--MLTSNRK	182
		: : : : :	-----LITLSNRK	182
Dd	108	ENSF--EPMKGQONPDIAAHV-----	ISEASSKTTSVLQAMEKGYTSSNNLVLENRK	159
Oy	183	-LRVNODGFYLYLANICF-RHHETSGSV	PPTDYLQLMWVVKTSIKIPSSHN--LMKGSST	238
		: : : : :	-----LMKGSST	238
Dd	160	GLTVKRQGGLIYIYAQTFTCSNREASSQ	AQP-----FLASLCMSPGFERILLRAANT	211
Oy	239	KWMSGNSEHFHSINVGGFFKLPAAGEISI	OVSNSPLDDPDODATYGAFKV	290
		: : : : :	-----	
Dd	212	H--SSAKPCGOOSIHLGVEFELQPGA	SVEFNVTDPQSOSHGTGTFISFGLLKL	261
RESULT	6			
S21738		CD40 ligand - mouse		
C:Species:	Mus musculus	(house mouse)		
C>Date:	31-Dec-1993	#sequence_revision 31-Dec-1993	#text_change 05-Nov-1999	
C:Accession:	S21738			
R:Amntage,	R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff			
: Cosman, D.; Spriggs, M.K.				
Nature	357, 80-82, 1992			
A:Title:	Molecular and biological characterization of a murine ligand for CD40.			
A:Reference number:	S21738; MUID:92244364			
A:Accession:	S21738			
A:Molecule type:	mRNA			
A:Residues:	1-260 <ARM>			
A:Cross-references:	EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PTD:g50352			
C:Keywords:	glycoprotein; transmembrane protein			
F:23-46/Domain:	transmembrane #status predicted <TM>			
F:47-260/Domain:	extracellular #status predicted <EXT>			
F:239/Binding site:	carbohydrate (asn) (covalent) #status predicted			
Query Match	9.8%; Score 153; DB 2; Length 260;			
Best Local Similarity	24.7%; Pred. No. 1.7e-05;			
Matches	73; Conservative 52; Mismatches 113; Indels 58; Gaps 15;			
Oy	10	PAPSAPARPPRAASKMFLALLGLGL-GQVCSIALFLYFRQMDPNRISDSHTCFYR	68	
		: : : : :	-----	
Dd	8	PPSRVATGLP--ASKRMVLTFLVLIQMIGSVFAVYLHRRDL--KVEEP-----	56	
Oy	69	IURLHEN----ADLDQSTLESDTLPDSCRRMKOAQOAVO-----	KELQHTVGPQRFSG	119
		: : : : :	-----	
Dd	57	-VNIHDEPFYFIKKLRCKNGEGSSLINCCEMRROFEDYIKDTLTKF-----	103	
Oy	120	APAMMGSLMDVAORGPPEAOPFAHLITINAS	IPSGSHKYVLSSMYHDRCAGAKISNM-T	178
		: : : : :	-----	
Dd	104	--EKKNSEF--EMQRDEDDEPQIAAHVSEA-----	NSNAASYLQMAKKGYTMKSNIJLVML	154
Oy	179	SNCK-LRVNODGFYLYLANICF-RHHETSGSV	PPTDYLQLMWVVKTSIR--IPSSHNLMLK	234
		: : : : :	-----	
Dd	155	ENGKOLTVAREGLYYVYQVTCFCSNREPSSQRP-----	PIVGIMLKPSIGSERILTK	206
Oy	235	GSGTKMSGNSEHFHSINVGGFFKLPAAGEISI	OVSNSPLDDPDODATYGAFKV	290
		: : : : :	-----	
Dd	207	AANTHSSSOLCDOQ--SVNLGCVFELQAGASVFVNTEASOVYTHRGVSPFGLKL	260	
RESULT	7			
J01344		tumor necrosis factor alpha precursor - horse		
N:Alternate names:	cachectin; TNF alpha			
C:Species:	Equus caballus (domestic horse)			
C>Date:	10-Sep-1999	#sequence_revision 10-Sep-1999	#text_change 04-Feb-2000	
C:Accession:	J01344			
R:Su, X.; Morris, D.D.; McGraw, R.A.				
Gene	107, 319-321, 1991			

A>Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis
A:Reference number: J01344; MUID:92084125

A:Accession: J01344

A:Molecule type: DNA

A:Residues: 1-234 <SD>

A:Cross-references: GB:M64087; NID:g164244; PIDD:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxicin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
E:78-234/Product: tumor necrosis factor alpha #status predicted <TM>
F:19_20/Binding site: myristate (Iys) (covalent) #status predicted
F:82/Binding site: carbonylrate (Ser) (covalent) #status predicted
F:16-I78/Dissulfide Bonds: #status predicted

Query Match 9.5%, Score 149; DB 1; Length 234;
Best Local Similarity 24.1%; Pred. No. 3,2e-05;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

OY I11 IVGPRFGAPAMMGSMILVAQRK-----PEAQFAHLITMAASIPSGHKVTLSSWY 165
 ::::| | : : : | : : || : : | : : | : : | : : | : :
DB 55 VIGPQREEDLPNAFG-STINPLAQTLRSSRTPSPDKPVAAVVAN----PQAEGQL---QWL 106

OY 166 HDGRMAKSIN-MTSLNGRLRVNODGEFYLYIANICFRHNETSGSVPTDLOLMVYYVKTSI 224
 : : : : : | : : : | : : | : : | : : | : : | : : | : :
DB 107 SGRNALALLANGKYKLTDNOVLVPDLGLYLISGVLFK----GGCGSTHYLLTHITSRIAY 162

OY 225 KIPSSHNLMKG-----GSTKMMSGNSEHFHSINYGFELKLRAGEEISTIOYSN 272
 | : : | : : | : : | : : | : : | : : | : : | : :
DB 163 SYPSRYNNLISAIKSPCHTESPPQAEAKPM-----YPPIYGVGFLKEKDQSIAETIQ 215

OY 273 PSLLD-PPODATTFYG 286
 | : : | : : | : : | : : | : : | : : | : : | : :
DB 216 PNVLDPAESGOVFYG 230

RESULT 8

COMSN

tumor necrosis factor alpha precursor - mouse

N:Alternate names: cachectin; TNF alpha

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000

C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R:Shiral, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988

A>Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A:Reference number: A22908; MUID:86224564

A:Accession: A22908

A:Molecule type: DNA

A:Residues: 1-235 <SH>

A:Cross-references: GB:M20155

Bioray. Khim. 13, 701-705, 1987

A>Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A:Reference number: S03791; MUID:87298639

A:Accession: S03791

A:Molecule type: DNA

A:Residues: 1-235 <SHA>

A:Cross-references: GB:M8296; NID:g202086; PIDD:AAAA04059.1; PID:g202087

A>Note: article in Russian with English abstract

R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
NuclAcids Res. 15, 9083-9084, 1987

A>Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nece
A:Reference number: A93679; MUID:88067722

A:Accession: A27303

A:Molecule type: DNA

A:Residues: 1-235 <SEM>

A:Cross-references: GB:Y00467; NID:g54830; PIDD:CAA6850.1; PID:g54832

R:Pernica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985

```

A>Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor
A:Reference number: A25164; MUID:85298296
A:Accession: A25164
A:Molecule type: mRNA
A:Residues: 1-235 <P>
R:Cross-references: GB:MI1731; NID:g202084; PIDN:AAA40458.1; PID:g202085
R:Fransen, L.; Muller, R.; Marmenolt, A.; Tavernier, J.; van der Heyden, J.; Kawashima
Nucleic Acids Res. 13, 4417-4429, 1985
A>Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression
A:Reference number: A23127; MUID:85242112
A:Accession: A23127
A:Molecule type: mRNA
A:Residues: 1-235 <F>
A:Cross-references: GB:X02611; NID:g548444; PIDN:CAA26457.1; PID:g54845
R:Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A>Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide result
A:Reference number: A34251; MUID:89380231
A:Accession: A34251
A:Molecule type: protein
A:Residues: 70-87 <CS>
R:Capit, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A>Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A:Reference number: I59058; MUID:86149365
A:Accession: I59058
A:Molecule type: mRNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-230,'R',232-235 <RES>
A:Cross-references: GB:MI3049; NID:g202082; PIDN:AAA40457.1; PID:g202083
R:Sherry, B.; Jue, D.W.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A>Title: Characterization of high molecular weight glycosylated forms of murine tumor
A:Reference number: A3696; MUID:91097531
A:Accession: A3696
A:Molecule type: protein
A:Residues: 80-85,'X',87-99 <SHE>
C:Genetics:
A:introns: 62/3; 81/1, 97/1
A>Note: The first intron occurs in the 5'-untranslated region
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F:80-235/Product: tumor necrosis factor #status experimental <MAT>
F:84/Binding site: myristate (lys) (covalent) #status predicted
F:86/Binding site: carbonylate (Ser) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted

```



```

DB      158  RFAVSYQTKWYNLLSAIKSPQGRTEPEGAAKPFW-----XEPYLGWFOLEKGRDLRST 210
OY      269  QVSNPSLDD-PDODATYFEG 286
      ::: 1: 11 : 111
DB      211  EIMLPAYLDFAESGQVYFEG 229

RESULT  12

OMHUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (hman)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S96153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
Nucleic Acids Res. 13, 6361-6373, 1985
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr
A:Reference number: A93585; MUID:86016093
A:Accession: A93585
A:Molecule type: DNA
A:Residues: 1-233 <END>
A:Cross-references: GB:X02910; GB:X02159; NID:q37209; PIDN:CAA26669.1; PID:q37210
R:Riris, F.J.M.; Bouquelieret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the Nkappab family within a
A:Reference number: S36152; MUID:93272029
A:Accession: S36153
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <RID>
A:Cross-references: EMBL:Z15026; NID:q37211; PIDN:CAA78745.1; PID:q37212
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pennica, D.; Nedwin, G.E.; Haylick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to
A:Reference number: A93351; MUID:85086244
A:Accession: A93351
A:Molecule type: mRNA
A:Residues: 1-233 <PND>
A:Cross-references: GB:X02910; GB:X02159; NID:q37209; PIDN:CAA26669.1; PID:q37210
A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promyeloid
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lan, L.S.; Strickler, J.; Van Arsdel, J.N.; AC
Science 228, 149-154, 1985
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A:Reference number: A44189; MUID:85142190
A:Accession: A44189
A:Molecule type: mRNA
A:Residues: 1-62, 'S', '64-233 <MAN>
A:Cross-references: GB:M10968; NID:q339737; PIDN:AAA61198.1; PID:q339738
R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; AC
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, beta and
A:Reference number: A61478; MUID:88301617
A:Accession: B61478
A:Molecule type: protein
A:Residues: 83-102;109-119;121-128, 'X', '130-131;142-144, 'X', '146, 'XXX', '150-152;159-174,186
R:Marmontou, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A:Reference number: I53311; MUID:86030296
A:Accession: I53311
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-233 <MAN>
A:Cross-references: GB:M26331; NID:q339763; PIDN:AAA36758.1; PID:q339764
A:Experimental source: U-937 cells
R:Takakura-Yamamoto, K.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A:Title: O-Glycosylated species of natural human tumor necrosis factor-alpha.
A:Reference number: S62610; MUID:96202967
A:Accession: S62610
A:Molecule type: protein
A:Residues: 77-99 <TAK>

```

R.i/D./Allonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A.Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
A.Reference number: I54522; MUID:94102809
A.Accession: I54522
A.Status: preliminary; translated from GB/EMBL/DBDB
A.Molecule type: DNA
A.Residues: 1-8 <DAL>
A.Cross-references: GB:S68530; NID:g544751
R.Stevenson, F.T.; Birsten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A.Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
A.Reference number: A59163; MUID:93018820
A.Contents: annotation; identification of myristylated lysines
R.Agarwal, B.B.; Kohr, W.U.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, S.A.; Br
J. Biol. Chem. 260, 2345-2354, 1985
A.Title: Human tumor necrosis factor. Production, purification, and characterization.
A.Reference number: A92511; MUID:65130974
A.Contents: annotation; disulfide bond
C.Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
out detriment to normal cells. It can also act synergistically with interferon gamma
C.Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
ut are produced by different cell types and have different induction kinetics.
C.Genetics:
A.Gene: GDB:TNF; TNFA
A.Cross-references: GDB:I20441; OMIM:191160
A.Map position: 6p21.3-6p21.3
A.Introns: 62/3; 78/1; 94/1
C.Complex: homotrimer
C.Superfamily: tumor necrosis factor
C.Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
F.1-76/Domain: propeptide #status predicted <PRO>
F.77-233/Product: tumor necrosis factor #status experimental <MAT>
F.19_20/Binding site: myristate (Lys) (covalent) #status experimental
F.81/Binding site: carbonydate (Ser) (covalent) (partial) #status experimental
F.145-177/Disulfide bonds: #status experimental

```

Query Match similarity: 8.9%; Score 139.5; DB 1; Length 233;
Best Local Similarity: 224.9%; Pred. No. 0.0002;
Matches 48; Conservative 34; Mismatches 76; Indels 35; Gaps 9;

Oy      111  IVGPOFSGAPMMEGSWLDVAQRK---PEAQPAHLITINAASPSSHKYTLSSWVHD 167
          ::|||::|
Db       55  VIGPOFEEPRDLSTLSPLAQAVRSSRTPSDKPAHVAVN---PQAEGL--QMLNR 107
          ::|||::|

Oy      168  RGAKTISN-MTSLNGKLRVNOGFEYLYANICFRHHETSGSVPTDYQL-----MY 218
          :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      108  RANALLANGVELRDNDLYVPSGIVLYITSQVLFK---GQGPSTHYLLTHITISRIASV 163

Oy      219  VVK---TSIKIPSSHNLKKGSGTKNWSGNSFEHFYSINVGFFFLRAGEELSIQVNS 274
          ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      164  QTEVNLISAKSCQREPRTEGAERKFW-----YEPILYGGVFLQEDKRLSRIENRP 216
          ||::|::|

Oy      275  ILD-PPQDATYFG 286
          ||::|

Db      217  YLDFAESGVYFG 229

RESULT 13
A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; U50727
R:ItO, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for
A:Reference number: A25454; MUID:86219711
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <ITO>

```

A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
 DNA 5, 157-165, 1986
 A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A:Reference number: A25451; MUID:86219712
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <IT2>
 A:Note: this sequence differs from that shown in having a Gln inserted between residues
 R:Shakhov, A.N.; Kuprash, D.V.; Azarov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
 A:Reference number: JH0309; MUID:91065534
 A:Accession: J50727
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues: 1-62, 'O', 63-234 <SHA>
 A:Cross-references: GB:M60340; GB:M5326; NID:g165754; PIDN:AAA31484.1; PID:g165756
 C:Genetics: 62/3; 80/1; 96/1
 A:introns: 62/3; 80/1; 96/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
 F:1-81/Domain: propeptide #status predicted <PRO>
 F:82-234/Product: tumor necrosis factor #status predicted <MAT>
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted
 F:83/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:147-178/Disulfide bonds: #status predicted

Query Match 8.8%; Score 137.5; DB 1; Length 234;
 Best Local Similarity 22.6%; Pred. No. 0.0003;
 Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

OY 5 EGPHPAPAPAPAPAPASR-----SFWLLGLGLGVVCSIALFLYFRAQMPNRIS 59
 |||||
 DB 14 EGPPL-----PKKAGPGGSKRCLISFLSFLVAGATTLC-----LHFVIGPGQERES 63
 OY 60 EOSTCFYRLRLHFNADLODSTLESDTLPSCKRMQAQVAGVOKLOHIVGQRRSG 119
 |||||
 DB 64 PNNLLV-----NPAQAVTLLS-----ASRALSDKPLAHV----- 95
 OY 120 APAMEGSLDVAQRGKPEAPFAHLITNAASIPSGSHKVTLLSMDHRGMAKISN-MTL 178
 |||||
 DB 96 ANPQVEG-----LQWLSRAAALLANGMKL 121
 OY 179 SNGKRVNODGFYLYANICRHHETSGSVPTDYLQLVVYVKSIRKIPSSHNMKG--- 235
 |||||
 DB 122 TDNQLVVPADGLYLYSQVLF-----SGGCRSYVLLTHFVSRAVSPYKVNKLLSAIKS 176
 OY 236 -----GSTKMSGSEFHFYSINVGPFKLRAGEISIOVNSPLD-PPQDATYF 285
 |||||
 DB 177 PCHRETPPEAPPMW-----YEPYLGAVFQLEKGRLESTEVNAPYLDLAEQGYVF 229
 OY 286 G 286
 |||||
 DB 230 G 230

RESULT 14
 154490
 Tumor necrosis factor alpha precursor - white-footed mouse
 C:Species: Peromyscus leucopus (white-footed mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
 C:Accession: 154490
 R:Crew, M.D.; Filipowsky, M.E.
 Immunogenetics 35, 351-353, 1992
 A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc
 A:Reference number: 154490; MUID:92218012
 A:Accession: 154490
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-235 <RES>
 A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:
 A:Gene: P1TNF
 A:introns: 62/3; 81/1; 97/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.7%; Score 135.5; DB 2; Length 235;
 Best Local Similarity 25.1%; Pred. No. 0.00045;
 Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

OY 111 IVGPORFSGAP-----AMMEGSLDVAQRGKPEAPFAHLITNAASIPSGSHKVTLS 163
 |||||
 DB 55 VIGPQREKFPNNPLITGSMAQTLLRSSQSSD-KPAHVAN-----HQVDEQL 105
 OY 164 WYHDGMAKISNMTLSNG-KLRVNO-----DGFYVLYANICFRHHETSGVPPDYDQLMV 217
 |||||
 DB 106 EWLNRG-----ANALLANGMDLKDQVLIPADGLVLYSQVLEKGGGSSVY-----LIT 155
 OY 218 YVVK-----TSIKIPSSHNMKGSTKNNSGSEFHFYSINVGPFKLRAGE 264
 |||||
 DB 156 HTVSRAVSYEDKYNLLSAIKSPCKEPPEGSSELKPM-----YEPYLGAVFQLEKGD 208
 OY 265 EISIOVNSPLD-PPQDATYFG 286
 |||||
 DB 209 RLSAEVLNPKYLDPAESGQYVFG 231

RESULT 15
 524642
 Tumor necrosis factor alpha precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: 146047; S24642
 R:Cludes, I.; Cleuter, Y.; Ketmann, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
 A:Reference number: 146046; MUID:94083525
 A:Accession: 146047
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-233 <CL2>
 A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798
 C:Genetics:
 A:Gene: TNFA
 A:introns: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:20/Binding site: myristate (lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 8.6%; Score 133.5; DB 1; Length 233;
 Best Local Similarity 25.8%; Pred. No. 0.00066;
 Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

OY 111 IVGPORFSGAP-----AMMEGSLDVAQRGKPEAPFAHLITNAASIPSGSHKVTLS 165
 |||||
 DB 55 VIGPQREKFPNNPLITGSMAQTLLRSSQSSD-KPAHVAN-----INSFG 100
 OY 166 HDGMAKISNMTLSNG-KLRVNO-----DGFYVLYANICFRHH-----ETSGSV 209
 |||||
 DB 101 QLRMDSYANALMANGVKLEDNQLVVPADGLYLYSQVLFROGQCPSTPLFTHTISRA 160
 OY 210 TDYQLMVYVTSIKIPSSHNMKGSTKNNSGSEFHFYSINVGPFKLRAGEISIQ 269
 |||||
 DB 161 VSY-QTRKNIL-SAIKSPCHRETPPEAEKPM-----YEPYLGAVFQLEKGRLSAE 211
 |||||
 OY 270 VSNPSLD-PPQDATYFG 286
 |||||

Tue Jul 9 13:21:01 2002

us-09-865-363-11.rpt

Page 8

Db 212 INLPDYLDVAESGQVFG 229

Search completed: July 8, 2002, 20:02:22
Job time: 4231 sec

RA "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ikeda T.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (potential).
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC TRABECULAR BONE AND LUNG.
CC -I- DISEASE: DEFICIENCY IN TNFSF1 RESULTS IN FAILURE TO FORM LOBULO-
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC OF NEONBORN. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPELOSIS, WITH
CC NO OSTEOCYLASTS, MARROW SPACES, OR TOOTH EKEPTION, AND EXHIBIT
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC HYPERCHROMATIC CHONDROCYTES.
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AF053713; AAC40113.1; -
DR EMBL; AF013170; AAC71061.1; -
DR EMBL; AB008426; BAA25425.1; -
DR EMBL; AF019048; AAB68812.1; -
DR EMBL; AB036798; BAA97259.1; -
DR MGD; MG1:1100089; Trfscfl.
DR InterPro; IPR003263; TNF_5
DR InterPro; IPR00478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR Prodom; PD008600; TNF_5; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PSS0049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KM Signal-anchor.
KN CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1 48 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT FT DOMAIN 49 69
FT FT TRANSMEM
FT FT
FT FT
FT FT
DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT CAROXYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROXYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 99 99 G -> D (IN REF. 4).
FT CONFLICT 99 99
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match 99.6%; Score 1554; DB 1; Length 316;
Best Local Similarity 99.7%; Pred. No. 3..9e-127;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

Oy	121	PAMGEGSMILDVARGRKEPEQOPRAHLLTINAAISPSGSHKVTLLSSMYHDPGRAKASNNLTSLN	180
Db	143	PAMGEGSMILDVARGRKEPEQOPRAHLLTINAAISPSGSHKVTLLSSMYHDPGRAKASNNLTSLN	202
Oy	181	GKLIVNDGDGYLYLYANICFRHHETSGSVPTDYLQMLVYVTKTSIKIPSSHNLMKGGSTYN	240
Db	203	GKLIVNDGDGYLYLYANICFRHHETSGSVPTDYLQMLVYVTKTSIKIPSSHNLMKGGSTYN	262
Oy	241	MSGNSEHFHSYIVNGGFEFKLRAGEEELSTIOVNSPILDDPDQATYEGAFKQYDID	294
Db	263	MSGNSEHFHSYIVNGGFEFKLRAGEEELSTIOVNSPILDDPDQATYEGAFKQYDID	316
RESULT 2			
TN1L	HUMAN	STANDARD:	PRT: 317 AA.
ID	TN1L_HUMAN	014788; 014723; 09P203;	
AC	16-OCT-2001	(Rel. 40, Created)	
DT	16-OCT-2001	(Rel. 40, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (osteoclast differentiation factor) (ODF).		
DE	TNFSF11 OR RANKL OR TRANCE OR OPGL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
NP	SEQUENCE FROM N.A.		
RC	TISSUE=Bone marrow; and Peripheral blood;		
RX	MEDLINE=96032977; PubMed=9367155;		
RA	Anderson T.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.,		
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."		
RL	Nature 390:175-179(1997).		
RN	[12]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph node;		
RX	MEDLINE=96827661; PubMed=9568710;		
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Bures T., Elliott R., Colombero A., Elliott G., Scully S., Sui L., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;		
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."		
RL	Cell 93:165-176(1998).		
RN	[13]		
RP	SEQUENCE OF 73-317 FROM N.A.		
RC	TISSUE=Thymocytes;		
RX	MEDLINE=97460112; PubMed=931213;		
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;		
RT	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."		
RL	J. Biol. Chem. 272:25190-25194(1997).		
RN	[14]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RC	TISSUE= tongue;		
RX	MEDLINE=20175237; PubMed=10708588;		
RA	Nagai M., Kyakumoto S., Sato N.;		
RT	"Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation."		
RL	Biochem. Biophys. Res. Commun. 269:532-536(2000).		
CC	-1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR. AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS		
CC			

```

CC      BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC      REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC      AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC      HYPERALCAEMIA OF MALIGNANCY.
CC      -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC      SECRETED (ISOFORM 2).
CC      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/SODF; ARE
CC      PRODUCED BY ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC      WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC      PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC      -1- INDICATION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC      -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC      -----
CC      THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC      BETWEEN THE SWISS INSTITUTE OF BIOFORMATICS AND THE EMBL OUTSTATION -
CC      THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC      USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC      MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC      ENTRIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/
CC      OR SEND AN EMAIL TO license@isb-sib.ch)
CC      -----
CC      EMBL: AF019047; AAB96811.1; -
CC      EMBL: AF053712; AAC93731.1; -
CC      EMBL: AF013171; AAC51762.1; -
CC      EMBL: AB037599; BAA90488.1; -
CC      MTM: 602642; -
CC      DR      InterPro: IPR003263; TNF_5.
CC      DR      InterPro: IPR000478; TNF_family.
CC      DR      Pfam: PF00229; TNF_1.
CC      DR      ProDom: PD008600; TNF_5; 1.
CC      DR      SMART: SM00207; TNF_1.
CC      DR      PROSITE: PS00251; TNF_1. FALSE_NEG.
CC      DR      PROSITE: PS50049; TNF_2; 1.
CC      KM      Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
CC      Signal-anchor; Alternative splicing.
CC      FT      DOMAIN 1 47
CC      FT      TRANSMEM 48 68
CC      FT      CYTOPLASMIC (POTENTIAL).
CC      FT      SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
CC      FT      (POTENTIAL).
CC      FT      DOMAIN 69 317
CC      FT      CAROAND 171 171
CC      FT      CAROAND 171 171
CC      FT      CAROAND 198 198
CC      FT      VARSPLIC 1 73
CC      FT      CONFLICT 194 194
CC      FT      MISSING (IN ISOFORM 2).
CC      FT      A -> G (IN REF. 3).
CC      SQ      SEQUENCE 317 AA: 35478 MW: 766176446348097F CRC64;

```

ID	TN10_HUMAN	STANDARD:	PRT:	281 AA.
AC	P50591;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2L) (Apo-2L).			
GN	TNFSF10 OR TRAIL OR APO2L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96111955; PubMed=8777713;			
RX	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,			
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,			
RA	Goodwin R.G.;			
RT	"Identification and characterization of a new member of the TNF			
RT	family that induces apoptosis."			
RL	Immunity 3:673-682(1995).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=96278649; PubMed=8663110;			
RA	Pitti R.M., Masters S.A., Rupert S., Donahue C.J., Moore A.,			
RA	Ashkenazi A.;			
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor			
RT	necrosis factor cytokine family."			
RL	J. Biol. Chem. 271:12687-12690(1996).			
RN	[3]			
RX	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.			
RX	HMEDLINE=20017054; PubMed=10549288;			
RA	Homolwitz S.G., Christinger H.W., Fuh G., Ulsch M., O'Connell M.,			
RA	Kelley R.F., Ashkenazi A., de Vos A.M.;			
RT	"Triggering cell death: the crystal structure of Apo2L/TRAIL in a			
RT	complex with death receptor 5."			
RL	Mol. Cell 4:563-571(1999).			
RL	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.			
RX	PubMed=10542098;			
RA	Mongkolkeha P., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,			
RA	Jones E.Y., Screaton G.R.;			
RT	"Structure of the TRAIL-DR5 complex reveals mechanisms conferring			
RT	specificity in apoptotic initiation."			
RL	Nat. Struct. Biol. 6:1048-1053(1999).			
CC	-1- FUNCTION: INDUCES APOPTOSIS.			
CC	-1- SUBUNIT: HOMOTRIMER (POTENTIAL).			
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).			
CC	-1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG			
CC	AND PROSTATE.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; U37518; AAC50332.1; -			
DR	EMBL; U57059; AAB01233.1; -			
DR	MIM; 603598; -			
DR	PDB; 1D0G; 22-OCT-99.			
DR	PDB; 1D4V; 01-NOV-99.			
DR	InterPro; IPR003263; TNF_5.			
DR	InterPro; IPR003636; TNF_abc.			
DR	InterPro; IPR000478; TNF_family.			
DR	Pfam; PF00229; TNF; 1.			
DR	ProDom; PD008012; TNF_abc; 1.			
DR	ProDom; PD008600; TNF_5; 1.			


```
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Z48469; CAAB8363.1; -.
DR HSP: P29965; IALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine: Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 23 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT FT (POTENTIAL).
FT DISULFID 47 261 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 178 218 POTENTIAL.
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787ED CRC64;

Query Match 11.9%; Score 185.5; DB 1; Length 261;
Best Local Similarity 24.7%; Pred. No. 6.8e-09;
Matches 71; Conservative 54; Mismatches 122; Indels 41; Gaps 13;

OY 10 PAPAPAPAPAPASRSMFLALLGLGIGVCSIALF-LYRAQMDPRISDESHCYR 68
DB 8 PPSRVAAGPP-VSMKFTLLVFLITOMIGSALFVYHRRDKIE-DEMNHEDFV 64
OY 69 ILRLHENADLQDSTLESDTLPSDCRRMKAQFOGAVOKELOHVQPFSGAPAMEGSW 128
DB 65 FMKTIQRCNKEGSLSL-NOEILRSRFEDLVKIDMON-KVKKKENFE--- 112
OY 129 LDVAQRGPEQAPAHLTINASTPSGSHKVTLSWYHDKWAKISN-WTISNGK-LRV 185
DB 113 ---MHKGOEPQIAHV-----ISEASSKTSYLVQAPKGYTILSNLVLENGKOLAV 163
OY 186 NODGFYLYANICF-RHNETSGSVPTDYLQMLVYVVKTSIKIPSSH-N-LMKGGSTKMS 242
DB 164 KRQGFYITTYOVTCSNRETLQAP-----FIASICLSPSGSERILRLAANTH--S 213
OY 243 GNSEHFYSINVGFEFLRAGEEISIOVSNPSLDPDQATYFGAFKY 290
DB 214 SSKPGQGSIHILGVLQSGASVFNVTDPQVSHGTGFSFGLKL 261

RESULT 6
FAST_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FAS antigen ligand.
GN TNFSF6 OR APPLIG1 OR FASL.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Euthera; Rodentia; Sclurognathii; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
MD MEDLINE=94084792; PubMed=7505205;
```

```
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U03470; AAC52129.1; -.
DR HSP: P01375; ATSV.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine: Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
FT FT PRO-RICH.
FT DOMAIN 4 69 POLY-PRO.
FT DISULFID 45 58 BY SIMILARITY.
FT CARBOHYD 199 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match 11.4%; Score 177.5; DB 1; Length 278;
Best Local Similarity 23.0%; Pred. No. 3.6e-08;
Matches 70; Conservative 42; Mismatches 101; Indels 91; Gaps 12;

OY 3 PHEGRLPAPAPAPAPAP-----PAASRSMFLALLGLGIGVCSIALFV 48
DB 50 PPSPL-PPSPQPPPLPLPLKKNIDELMLVIFENVLVALVKGLS-----MYOL 101
OY 49 PRAQMDNRISDSSTHCFYILRLHENADLQDSTLESDTLPSDCRRMKAQFOGAVOKEL 108
DB 102 FHLQKELAELEFNTN-----SLRVSSFEKQINPSTPSTK----- 138
OY 109 OHIVQPRFGAPAMMGSWLDVAQRGPEQAPAHLTIN-AASTPSGSHKVTLSWYH 166
DB 139 -----KPRS--VAHLTGPRRSIP-----LEWED 161
OY 167 DRGMAKISNMTLSNGKLRYNODGFYLYANICFRHNETSGSVPTDYLQMLVYVVKTSIKI 226
DB 162 TYGTALISGVYKKKGLVINEAGLYFYYSKYVR-GQSCNSQP---LSHKVYV--RNFKY 215
OY 227 PSSHNLKMGSGTKMNSGNSEHFYSINVGFEFLRAGEEISIOVSNPSLDPDQATYFG 286
```

Db 216 PGDLVME-EKKLVCTTGQIWAHSSYIGAVENLTVDHLTVNTLSQSLNFEESKTFPG 274
OY 287 AFKV 290
Db 275 LYKL 278

RESULT 7
FASTL MOUSE STANDARD: PRT: 279 AA.
ID FASTL MOUSE
PA1047: 061217: 09RIF2:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FAS antigen ligand.
GN TNFSF6 OR APRIL1 OR FASL OR GLD.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RX STRAIN=C57BL/6;
MEDLINE=95386076; PubMed=7544870;
RA Peltsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=789405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=BALB/C;
RA Fener M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids.";
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX STRAIN=C3H; Tissue=Spleen;
MEDLINE=20021694; PubMed=10552956;
RA Ayroldi E., Adamio F., Zollo O., Agostini M., Moraca R.,
RA Cananali L., Migliorati G., Delino D.V., Riccardi C.;
RT "Cloning and expression of a short Fas ligand: A new alternatively
RT spliced product of the mouse Fas ligand gene.";
RL Blood 94:3456-3467(1999).
RN [6]
RP CHARACTERIZATION OF VARIANT GLD.
RX MEDLINE=96091792; PubMed=7495745;
RA Hahne M., Peltsch M.C., Imler M., Schroeter M., Lowin B.,
RA Ransau M., Bron C., Renno T., French L., Tschopp J.;
RT "Characterization of the non-functional Fas ligand of gld mice.";
RL Int. Immunol. 7:1381-1386(1995).
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE

CC T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
CC ISOFORM FASL IS SOLUBLE.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
CC INTERACTION.
CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: U06948; AAA17800.1; -;
DR EMBL: U10984; AAA19778.1; -;
DR EMBL: S76752; AAB33780.1; -;
DR EMBL: U58995; AAB02915.1; -;
DR EMBL: AF119335; AAD52106.1; -;
DR HSSP: P01375; 4TSV.
DR MCD; MGI:99255; Tnfef6.
DR InterPro; IPR003263; TNF-5.
DR InterPro; IPR003636; TNF-abc.
DR InterPro; IPR000478; TNF-family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF-abc; 1.
DR ProDom; PD008600; TNF-5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF-1; 1.
DR PROSITE; PS50049; TNF-2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
KW Disease mutation; Alternative splicing.
FT DOMAIN 1 78
FT TRANSMM 79 100
FT DOMAIN 101 279
FT DOMAIN 4 69
FT DOMAIN 51
FT DISULFD 200 231
FT CARBOHYD 117 117
FT CARBOHYD 182 182
FT CARBOHYD 248 248
FT VARSPLIC 1 210
FT VARIANT 184 184
FT VARIANT 218 218
FT VARIANT 273 273
SQ SEQUENCE 279 AA; 31442 MW; 37972B278E0A1CA CXC64;
TO ITS RECEPTOR).

Query Match 11.3%; Score 177; DB 1; Length 279;
Best Local Similarity 23.0%; Pred. No. 4e-08;
Matches 70; Conservative 46; Mismatches 97; Indels 92; Gaps 13;
OY 3 PHEGLHPAPAPAPAP-----PAAHSMFTALDGLGLGVVCSIALFL 47
Db 50 PVVSPPL-PEPSQPLPLPLPLPLKKKDHNTLMLPVVFVVALVALVGMGIG-----MYQ 101
OY 48 YRAQMDPKRIEDSDHCHYRLRLKLNENDLQDSTLESDETLDPDCRRKKAQFGAVQKE 107
Db 102 LPHLOKE---LAE-----LREFTNQSLKVVSEFKQIANPST----- 134
OY 108 LCHIVGPRFSGAPAMEGSWIDVAQRGKPEAPFAHLITN--AASIPSGSHKVLSSNY 165
Db 135 -----PSE-----KKERRSVAHLGNHNSIP-----LEWE 161

QY 166 HDGMAKISMTLSNCKLRVNDGFYLYANICFRHHTSGSVPTDYLQMLVYVYKTSIK 225
DB 162 DTYGATLISCVKRYKGGVLYNETGLYFVSKYFR--GSCNNPLNH---KYYM--RNSK 215
QY 226 IPSSHNLKMGKSTKMSGSEFHFYSINVGCFKLAGEISIQVNSPLDDQDQATF 285
DB 216 YPDDVLVME-EKRLNCTTGQTGMASHSSYLGAVERNLSADHLVYVNSQLINEESKTFE 274
QY 286 GAFKV 290
DB 275 GLYKL 279

RESULT 8
FAST_HUMAN STANDARD: PRT: 281 AA.
ID P48023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FAS antigen ligand (Apoptosis antigen ligand) (APTL) (CD178 antigen).
GN TNFSF6 OR APTL1G1 OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T lymphocytes".
RL J Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species specificity".
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Schaeuble C.E., Poehmann R., Philippen P., Ethel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA Fushimoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus infection".
RL Blochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP TISSUE=Blood;
RC Matsunuma M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL SURFACE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD178 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/3338769674.g.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: X89102; CAA61474.1; -
DB EMBL: U08137; AAC50071.1; -
DB EMBL: U11821; AAC50124.1; -
DB EMBL: D38122; BAA07320.1; -
DB EMBL: 296050; CAB09424.1; -
DB EMBL: AB013303; BAA32542.1; -
DB HSP; P06804; TNF.
DB MIM; 134638; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR003636; TNF_ab.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD002012; TNF_ab; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR SMART: SM00251; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 70 PRO-RICH.
FT DOMAIN 45 65 POLY-PRO.
FT DISULFID 202 233 BY SIMILARITY.
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 281 AA; 31485 MW; ABA6EB358246E9BB CRC64;

Query Match 11.18; Score 174; DB 1; Length 281;
Best Local Similarity 21.88; Pred. No. 7,4e-08;
Matches 67; Conservative 43; Mismatches 104; Indels 94; Gaps 10;

QY 3 PHEGRLPAPSPAPAP-----PPAASRS-----MFALLGLGIGVGVCSIA 44
DB 48 PPPPPPLPPPPPPPLPPLPLPLKRGKNSSTGLCLVFMVLAVALVGLG----- 100
QY 45 LELYFRAQMDPNRISEDSTNCFYRIILRLHENDLQDSTLESDTLDPSCRMRKQAFQAV 104
DB 101 MFOLFHLQ-----KELALRETSQMHTA-----SSL 127
QY 105 OKELQHIYVGPQRFSGAPAMMEGSLDYAQRKPEAPFAFLT--INAASTPSCSHVVTLS 162
DB 128 EKQIGHSPPE-----KKELRVVAHLTKSKNSRSP-----L 160
QY 163 SWYHRCMAKISMTLSNCKLRVNDGFYLYANICFRHHTSGSVPTDYLQMLVYVYKTSIK 225
DB 161 EMEYDYGIVLVKCVKRYKGGVLYNETGLYFVSKYFRGSCNN-----LPLSHVYKAR 214
QY 223 STIPSSHNLKMGKSTKMSGSEFHFYSINVGCFKLAGEISIQVNSPLDDQDQATF 285
DB 215 NSRYPDVLVME-GKMMSYCTTGGMARSSYLGAVERNLSADHLVYVNSQLINEESKTFE 274
QY 283 TYFGAFKV 290
DB 274 TFGGLYKL 281

RESULT 9
TNFS_HUMAN STANDARD: PRT: 261 AA.

AC P29965;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCN-2001 (Rel. 40, Last annotation update)
DE CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell
DE antigen gp39) (CD134 antigen).
GN TNFSF5 OR CD40LG OR CD40L OR TRAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93076854; PubMed=1280226;
RA Graf D., Korthauer U., Mages H.W., Senger G., Kroccek R.A.;
RT "Cloning of TRAP, a ligand for CD40 on human T cells.";
RL Eur. J. Immunol. 22:3191-3194(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93049181; PubMed=1385114;
RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
RA Briesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
RA Aruffo A.;
RT "The human T cell antigen gp39, a member of the TNF gene family, is a
RT ligand for the CD40 receptor: expression of a soluble form of gp39
RT with B cell co-stimulatory activity.";
RL EMBO J. 11:4313-4321(1992).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.
RX MEDLINE=93145530; PubMed=7678782;
RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Mlatovich A.,
RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,
RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;
RT "The CD40 ligand, gp39, is defective in activated T cells from
RT patients with X-linked hyper-IgM syndrome.";
RL Cell 72:291-300(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93094757; PubMed=1281209;
RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,
RA Macculif B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
RT "Recombinant human CD40 ligand stimulates B cell proliferation and
RT immunoglobulin E secretion.";
RL J. Exp. Med. 176:1543-1550(1992).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=93138085; PubMed=7678552;
RA Gauchat J.F.M., Aubry J., Mazzei G.J., Ilie P., Jomotte T., Elson G.,
RA Bonnefoy J.Y.;
RT "Human CD40-ligand: molecular cloning, cellular distribution and
RT regulation of expression by factors controlling IgE production.";
RL FEBS Lett. 313:259-266(1993).
RN [6]
RP SEQUENCE FROM N.A.
RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
RA Matsuda I.;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
RX MEDLINE=96131874; PubMed=859998;
RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
RA Chess L., Thomas D.;
RT "2-A crystal structure of an extracellular fragment of human CD40
RT ligand.";
RL Structure 3:1031-1039(1995).
RN [8]
RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
RX MEDLINE=9826353; PubMed=9605317;
RA Shieh J., Garber E., van Viljmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).

RN [9]
RP VARIANTS HIGM1 ARG-36 AND GLY-140.
RX MEDLINE=93156839; PubMed=7679206;
RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
RA Kroccek R.A.;
RT "Defective expression of T-cell CD40 ligand causes X-linked
RT immunodeficiency with hyper-IgM.";
RL Nature 361:539-541(1993).
RN [10]
RP VARIANT HIGM1 GLU-123.
RX MEDLINE=93156840; PubMed=8094231;
RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
RA de Saint Basile G.;
RT "CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM.";
RL Nature 361:541-543(1993).
RN [11]
RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
RX MEDLINE=93174270; PubMed=7679801;
RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
RA Copeland N.G., Bedell M.A., Edlhoft S., Distèche C.M.,
RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;
RT "CD40 ligand gene defects responsible for X-linked hyper-IgM
RT syndrome.";
RL Science 259:990-993(1993).
RN [12]
RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
RX MEDLINE=9523438; PubMed=7717401;
RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoti D.,
RA Gillani S., Mantuano E., Fasch A., Andersson B., Zegers B.J.M.,
RA Cavaiani G., Reznick I., Levy J., Zan-Bar I., Porat Y., Alro P.,
RA Plebani A., Vezzoni P., Notarangelo L.D.;
RT "Characterization of nine novel mutations in the CD40 ligand gene in
RT patients with X-linked hyper IgM syndrome of various ancestry.";
RL Am. J. Hum. Genet. 56:898-906(1995).
RN [13]
RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
RX MEDLINE=96133533; PubMed=8550833;
RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
RA Gatti R.A., Deruff D.C., Belmont J.W., Conley M.E.;
RT "A single strand conformation polymorphism study of CD40 ligand.
RT Efficient mutation analysis and carrier detection for X-linked hyper
RT IgM syndrome.";
RL J. Clin. Invest. 97:196-201(1996).
RN [14]
RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
RX MEDLINE=97295077; PubMed=9150729;
RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,
RA Yata J.-I., Ochs H.D.;
RT "Mutations of the CD40 ligand gene in 13 Japanese patients with
RT X-linked hyper-IgM syndrome.";
RL Hum. Genet. 99:624-627(1997).
RN [15]
RP FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
RN STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
RN INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
RN SUBUNIT: HOMOTRIMER.
RN SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
RN EXTRACELLULAR SOLUBLE FORM.
RN TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
RN T-LYMPHOCYTES.
RN DISEASE: DEFECTS IN TNFSF5 ARE THE CAUSE OF AN X-LINKED
RN IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1). AN IMMUNOGLOBULIN ISOTYPE
RN SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
RN IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
RN PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
RN RECURRENT BACTERIAL AND OPURTUNISTIC INFECTIONS, INCLUDING
RN PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
RN CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
RN INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
RN WITH A DEATH RATE OF ABOUT 10% BEFORE ADULESCENCE.
RN SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
RN DATABASE: NAMB=CD40dbase;
RN NOTE-European CD40L defect database (mutation db);


```

CC WWW="http://www.expasy.org/cdd401base/";
CC FTP="ftp://ftp.expasy.org/databases/cdd401base";
CC -1 DATABASE: NAME=PROV; NOTE=CD guide CD154 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/ncbi/cdd/cdd401base.htm"
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X68550: CAA48554.1; -
DR EMBL: 215017: CAA78737.1; -
DR EMBL: X67878: CAA48077.1; -
DR EMBL: L07414: AAA35662.1; -
DR EMBL: D31797: BAA06599.1; -
DR EMBL: D31793: BAA06599.1; JOINED.
DR EMBL: D31794: BAA06599.1; JOINED.
DR EMBL: D31795: BAA06599.1; JOINED.
DR EMBL: D31796: BAA06599.1; JOINED.
DR PIR: S26684: S26684.
DR PIR: S26694: S26694.
DR PIR: S28017: S28017.
DR PIR: S28852: S28852.
DR PIR: JH0793: JH0793.
DR PDB: 1ALY: 17-SEP-97.
DR MIM: 308230: -
DR InterPro: IPR003263: TNF_5.
DR InterPro: IPR000478: TNF_family.
DR Pfam: PF00229: TNF_1.
DR ProDom: PD008600: TNF_5; 1.
DR SMART: SM00207: TNF_1.
DR PROSITE: PS00251: TNF_1; 1.
DR PROSITE: PS50049: TNF_2; 1.
DR CytoKine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
KW Domain; Disease mutation; Polymorphism.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
FT DISULFID 178 216 POTENTIAL.
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 36 36 M -> R (IN HIGM1).
FT VARIANT 123 123 A -> E (IN HIGM1).
FT VARIANT 126 126 V -> A (IN HIGM1).
FT VARIANT 128 129 /FTID-VAR_007515.
FT VARIANT 140 140 SE -> RG (IN HIGM1).
FT VARIANT 140 140 /FTID-VAR_007516.
FT VARIANT 140 140 W -> C (IN HIGM1).
Query Match 10.9%; Score 169.5; DB 1; Length 261;
Best Local Similarity 25.7%; Pred. No. 1.6e-07;
Matches 75; Conservative 50; Mismatches 116; Indels 51; Gaps 16;

```

```

OY 239 KMGSGNEPHRYSTINVGGEFFKAGEEISTQVNSPLDDPDQATYRGARKV 290
DB 212 H--SSAKPCGQSTHILGVEFELPGASVFNWYDPSVSHGTGFTSGLKL 261
RESULT 10
TNF5_FELCA STANDARD; PRT; 260 AA.
AC 097605;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand (CD154 antigen).
GN TNFSP5 OR CD40LG OR CD40L.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_Taxid=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Hosie M.J., Willett B.J.;
RT "Adjuvant properties of feline CD154 (CD40 ligand).";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF079105: AAD02954.1; -
DR HSSP: P29965: 1ALY.
DR InterPro: IPR003263: TNF_5.
DR InterPro: IPR000478: TNF_family.
DR Pfam: PF00229: TNF_1.
DR ProDom: PD008600: TNF_5; 1.
DR SMART: SM00207: TNF_1.
DR PROSITE: PS00251: TNF_1; 1.
DR PROSITE: PS50049: TNF_2; 1.
DR CytoKine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
FT DISULFID 177 217 POTENTIAL.
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 260 AA; 28727 MW; 349FA0391FB7B32 CRC64;
Query Match 10.7%; Score 167; DB 1; Length 260;
Best Local Similarity 25.4%; Pred. No. 2.7e-07;
Matches 74; Conservative 50; Mismatches 117; Indels 50; Gaps 16;

```

```

DR 111 -----AMOKGQDPRVAHV-ISEAS-----SSTASVLQW-APKGYITSSMLVLENNKQ 159
DB 183 LRVNODGFYLLYANICF-RHHETSGSVPTDYLOLMVYVKTISKIPSSHN-LMKGGSTK 239
QY 160 LAVKROGLYIYAQVTFCSNRASQAP-----FIASLCHSPSGSEHVLRLAANAR 211
DB 240 NMSGNSEHFHSINVGCFKIRAGEEISIOVSNPSLDDPPDATTYFGAFKY 230
QY 212 -SSSKPCGQGSIHUGVFEFLHPGASVFVNVDPSQVSHGTSTFGLKL 260

RESULT 11
TNFA.CANFO STANDARD; PRT; 234 AA.
AC PS1435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (cachectin).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-Lung;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RA White A.W., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha."
RL Am. J. Physiol. 273:L524-L530(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U39839; AAB06492.1; -
DR EMBL: U77036; AAB19210.1; -
DR HSSP: P06804; 2TNF.
DR InterPro: IPR003636; TNF-abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRINTS: PR01234; TNCRSISICT.
DR PRODOM: PD002012; TNF-abc; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.

```

```

DR PROSITE: PS0049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 79 BY SIMILARITY.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 147 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 10.1%; Score 157; DB 1; Length 234;
Best Local Similarity 26.1%; Pred. No. 1.7e-06;
Matches 54; Conservative 26; Mismatches 65; Indels 62; Gaps 9;

QY 111 IVGPOR---FSGAPAMMGSWLVAORGRPEAQ-----PFAHLITNASIP 153
DB 55 VIGPQREQESSGPPF-----RPLAQTLIRASQNDNDKPVAVHANQQAEE 102
QY 154 SGSHKVTLSWYHGRGAKNSN-MTLNGLRVNODGFYLLYANICFRHHETSGSVPTDY 212
DB 103 E-----LQWLSKRAVALLANGMLSDNQLVPSDLTYLYISQVLPK-----GQGCPSY 150
QY 213 LQIMVYVKTISKIPSSINLM-----KGGSTKNMSGSEHFHSINVGFEKL 260
DB 151 LLTHVTSRLAVSYPEKYNLLSAIKSPQKETPEGAERKPW-----YEPITYLGVFOL 203
QY 261 RAGEEISIOVSNPSLDD-PPDATTYFG 286
DB 204 QKGDRLSAEVLNLPQYLDPAFADSGQIYFG 230

RESULT 12
TNFS.CANFA STANDARD; PRT; 260 AA.
ID TNFS.CANFA
AC 097626;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand.
GN TNFSF5 OR CD40LG OR CD40L.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willett B.J.;
RT "Adjutant properties of canine CD40L."
RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF086711; AAD04375.1; -
DR HSSP: P29965; 1ALY.
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR PRODOM: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS0049; TNF_2; 1.

```

KM Cytokine: Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 47 260 (POTENTIAL).
 FT DISULFID 177 217 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 239 239 POTENTIAL.
 SQ CAROHRD 260 AA: N-LINKED (GLCNAC. . .) (POTENTIAL).
 604F69A19E98EB70 CRC64;

Query Match 10.1%; Score 157; DB 1; Length 260;
 Best Local Similarity 25.5%; Pred. No. 2e-06;
 Matches 75; Conservative 50; Mismatches 113; Indels 56; Gaps 17;

QY 11 APSADAPAPAPASRSMELALIGLGLGVVCSIALF-LYFRAOM----DPNRISDSTHC 65
 DB 9 ABRSAVATGP--VSMKIFMYLTLVFLITOMIGSALFAVYLHRLDKIDENLYED--FV 64
 QY 66 FYRIIRLHFNADLDOSTLESDTLPDSRRMKOAFQGVOKELOHIVGPQRFSGAPAME 125
 DB 65 FPKTLQKCNKGGSLSL-----NCEIKSQPE-AFLKEIM-LNNEMKKEENIAM-- 112
 QY 126 GSWLDVAORGRPEAPFAHLITINASIPSGSHKVTLSWYHNRGMAKISN--MTLSNGK- 182
 DB 113 -----QKQODPRIAAHVISEASNP-----SVLRW-APKGYTTISMLVLENGKQ 159
 QY 163 LRVNODGFYLYANICF-RHHETSGSVPTDYQLQMLVYVVKTSIKIPSSH--LAKGSGTK 239
 DB 160 LAVKHQGLYVYAQVTFCSNRASQAQ-----FVASCLHSPSTEVLLRAASSR 211
 QY 240 MMS---GMSERHFSINCGFPRKAGEIIOVSNPSLDDPDADATYFGAFKV 290
 DB 212 GSKKPCGGO-----SHLGVEFLHFGASVFNVTDPQSQVSHGTGTFSGFLKL 260

RESULT 13
 TNFS_MOUSE STANDARD; PRT; 260 AA.
 AC P27548: 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen GP39)
 DE TNFS5 OR CD40LG OR CD40L.
 CN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92244364; PubMed=1374165;
 RA Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L.,
 RA Mochulski B.M., Anderson D.M., Gimpel S.D., Davis-Smith T.,
 RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
 RA Spriggs M.K.:
 "Molecular and biological characterization of a murine ligand for
 RT CD40.";
 RT Nature 357:80-82(1992).
 RL Nature 357:80-82(1992).
 RN [2]
 RP REVISION TO 199.
 RA Spriggs M.K.:
 RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SIMILARITY TO THE TNF FAMILY.
 RX MEDLINE=92310561; PubMed=1377364;
 RA Farrah T., Smith C.A.:
 RT "Emerging cytokine family."
 RL Nature 358:26-26(1992).
 RN [4]
 RP 3D-STRUCTURE MODELING OF 115-260.
 RX MEDLINE=93200072; PubMed=8095800;
 RA Peitsch M.C., Jongeneel C.V.;

RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer
 similar to the tumor necrosis factors.";
 RL Int. Immunol. 5:233-238(1993).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
 CC T-LYMPHOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL: X65453; CAA46448.2; .
 DR PIR: S21738; S21738.
 DR PDB: 1CDA; 31-OCT-93.
 DR MGD: MGI:88337; Tnf5f5.
 DR InterPro: IPR003263; Tnf5f5.
 DR InterPro: IPR000478; Tnf_family.
 DR Pfam: PF00229; Tnf_1.
 DR ProDom: PD008600; Tnf_5; 1.
 DR SMART: SM00207; Tnf_1.
 DR PROSITE: PS00251; Tnf_1; 1.
 DR PROSITE: PS50049; Tnf_2; 1.
 DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 46 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 47 260 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DISULFID 177 217 (POTENTIAL).
 FT CARBOHYD 239 239 POTENTIAL.
 SQ SEQUENCE 260 AA: 29370 MW: 7E1AC117473672AD CRC64;

Query Match 9.8%; Score 153; DB 1; Length 260;
 Best Local Similarity 24.9%; Pred. No. 4.4e-06;
 Matches 74; Conservative 53; Mismatches 110; Indels 60; Gaps 16;

QY 10 PASADAPAPAPASRSMELALIGLGLGVVCSIALF-LYFRAOMDPNRISDSTHCYVR 68
 DB 8 PSPRSVATGP--VSMKIFMYLTLVFLITOMIGSVLFAVYLHRLD--KYEE----- 56
 QY 69 ILRLHEN---ADLDOSTLESDTLPDSRRMKOAFQGVAVO-----KELOHIVGPQRFSG 119
 DB 57 -VNLHDEPFYIKKLKCNKGGSLSLNCEEMKROFEDLVKIDTLNKE----- 103
 QY 120 APAMGMSWLDVAORGRPEAPFAHLITINASIPSGSHKVTLSWYHNRGMAKISNM-T 178
 DB 104 --EKRENSF--EMQRGDEDEPQIAAHVSEA-----NSNAAVLQNAKKGYITMKSNLVL 154
 QY 179 SNKG-LRVNODGFYLYANICF-RHHETSGSVPTDYQLQMLVYVVKTSIKIPSSH--LM 233
 DB 155 ENKQLTVRREGLYVYVTVTFCSNRPSSORP-----FIVGLMK-PSSGSEIRLL 205
 QY 234 KGGSTKMGSGNSEHFYSINCGFPRKAGEIIOVSNPSLDDPDADATYFGAFKV 290
 DB 206 KAANTHSSSQLEQO--SVHLGVEFLQMGASVFNVTASOIVHRVGFSSGLLKL 260

RESULT 14
 TNFA_HORSE STANDARD; PRT; 234 AA.
 AC P29553: 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
 GN TNF OR TNFA.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NC NCBL-TaxID-9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92084125; PubMed-1748301;
 RA Su X., Morris D.D., McGraw R.A.;
 RT "Cloning and characterization of gene TNF alpha encoding equine tumor
 necrosis factor alpha.";
 RL Gene 107:319-321(1991).
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M64087; AAA30959.1; -.
 DR PIR: J01344; J01344.
 DR HSSP: P01375; 4T5V.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 KM PROPEP 1 77 BY SIMILARITY.
 FT CHAIN 78 234 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 146 178 BY SIMILARITY.
 FT SEQUENCE 234 AA; 25469 MW; E79AC91143DE373 CRC64;
 SQ
 Query Match 9.5%; Score 149; DB 1; Length 234;
 Best Local Similarity 24.1%; Pred. No. 8.5e-06;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

DB 216 PNLYDEASGQVYFG 230
 RESULT 15
 ID TNFA_MACEFA STANDARD; PRT; 233 AA.
 AC P79337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
 GN TNF OR TNFA.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 NC NCBL-TaxID-9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lymphocytes;
 RA Tatsumi M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDJ databases.
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CANCER AND INFECTIO, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB000513; BAA19131.1; -.
 DR HSSP: P01375; 4T5V.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 KM PROPEP 1 76 BY SIMILARITY.
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DISULFID 145 177 BY SIMILARITY.
 FT SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;
 SQ
 Query Match 9.5%; Score 148.5; DB 1; Length 233;
 Best Local Similarity 25.6%; Pred. No. 9.3e-06;
 Matches 50; Conservative 38; Mismatches 68; Indels 39; Gaps 11;

QY 166 HDGMAKISN-MTLSNGKLRVNODGFYLYANICERHETSGSVPTDYQL-----M 216
Db 106 NRRANALVANGVELTNDQLVVPSEGLYLIYSQVLEK---GOGCPSNHVLTHTTISRIV 161
QY 217 VYVVK---TSIKIPSSHNLKMGSGSTKNMGSSEPHFYSINVGCFPKLRAGEEISIOYSN 272
Db 162 SYOTKYNLSAISKPCQRETPGGAENKFW-----YEPYILGVGFQLEKGDRLSAEINTL 214
QY 273 PSLLD-PQODATYFG 286
Db 215 PDYLDFAESGQYVFG 229

Search completed: July 8, 2002, 18:51:49
Job time: 17487 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 16:22:56 ; Search time 119.9 Seconds
(without alignments)
424.191 Million cell updates/sec

Title: US-09-865-363-11

Perfect score: 1561
Sequence: 1 GVPHEGRLHPAPSAPAPAP.....LDDPDQDATYFGAFKQDID 294

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1525.5	97.7	313	11	Q9RIY0 mus musculus
2	1492	95.6	318	11	Q9SE22 rat mus musculus
3	1426	91.4	287	11	Q9JJK9 mus musculus
4	1227	78.6	270	4	Q96Q17 mus musculus
5	1057	67.7	199	11	Q9JJK8 mus musculus
6	272	17.4	53	11	Q9JJK8 mus musculus
7	263.5	16.9	214	13	Q9JJK8 mus musculus
8	218.5	14.0	287	13	Q9JJK8 mus musculus
9	186.5	11.6	261	6	Q9BDN3 mus musculus
10	180.5	11.5	280	6	Q9BDN3 mus musculus
11	179	11.3	280	6	Q9BDN3 mus musculus
12	177	11.3	280	6	Q9BDN3 mus musculus
13	175	11.2	261	6	Q9BDN1 mus musculus
14	174.5	11.2	261	6	Q9BDN1 mus musculus
15	173	11.1	282	6	Q9BDN1 mus musculus
16	172.5	11.1	272	13	Q918D8 mus musculus

17	172.5	11.1	282	6	Q9BEA8	Q9BEA8 sus scrofa
18	172.5	11.1	282	6	Q9SM04	Q9SM04 sus scrofa
19	152	9.7	240	6	Q9BDM7	Q9BDM7 macaca nemo
20	149	9.5	234	6	Q9TRJ3	Q9TRJ3 equus caball
21	148	9.5	232	11	Q35853	Q35853 mus musculus
22	147.5	9.4	310	11	Q9JMK10	Q9JMK10 macaca nem
23	143	9.2	260	11	Q9Z2V2	Q9Z2V2 rat mus mus
24	143	9.2	260	11	Q9R254	Q9R254 rat mus mus
25	142.5	9.1	239	11	Q9QYH9	Q9QYH9 mus musculu
26	142	9.1	232	4	Q9JMK11	Q9JMK11 macaca nem
27	140.5	9.0	310	11	Q9JMK11	Q9JMK11 macaca nem
28	140	9.0	174	4	Q9S150	Q9S150 homo sapien
29	139	8.9	234	6	Q9S150	Q9S150 capra hircu
30	136	8.7	191	6	Q9WY22	Q9WY22 capra hircu
31	133.5	8.6	215	11	Q9JND1	Q9JND1 tamiasciuru
32	133	8.5	157	4	Q43647	Q43647 homo sapien
33	132	8.5	149	6	Q97543	Q97543 actus nancy
34	132	8.5	217	11	Q9ERG6	Q9ERG6 actus nancy
35	131.5	8.4	156	11	Q91Z14	Q91Z14 sigmodon hl
36	131	8.4	149	6	Q97538	Q97538 actus vocif
37	131	8.4	149	6	Q97538	Q97538 actus vocif
38	130	8.3	204	4	Q96LD2	Q96LD2 homo sapien
39	130	8.3	204	4	Q96LD2	Q96LD2 homo sapien
40	128.5	8.2	233	6	Q9BEA1	Q9BEA1 mesocricetu
41	127.5	8.2	217	6	Q9BEC5	Q9BEC5 tenrec ecau
42	126.5	8.1	217	6	Q9BEG1	Q9BEG1 bradyptus tr
43	126.5	8.1	217	6	Q9BEG0	Q9BEG0 cyclops dl
44	126.5	8.1	250	6	Q9XT47	Q9XT47 macropus eu
45	126	8.1	216	6	Q9BEC9	Q9BEC9 ochotona pr

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	313 AA
Q9RIY0	Q9RIY0			
AC	Q9RIY0			
DT	01-MAY-2000 (TREMURel. 13, Created)			
DT	01-MAY-2000 (TREMURel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMURel. 19, Last annotation update)			
DE	OSTEOCLAST DIFFERENTIATION FACTOR.			
GN	TNFSF11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SYRAIN=129;			
RX	MEDLINE=99214075; PubMed=10196481;			
RA	Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,			
RT	Ueda M., Higashio K.,			
RT	"Cloning and characterization of the gene encoding mouse osteoclast			
RT	differentiation factor."			
RL	Gene 230:121-127(1999).			
DR	EMBL: AB022036; BAA36970.1; -			
DR	EMBL: AB022037; BAA36970.1; JOINED.			
DR	EMBL: AB022038; BAA36970.1; JOINED.			
DR	HSSP: P50591; IDOG.			
DR	MCD: MGI:1100089; Tnfsf11.			
DR	InterPro: IPR003263; TNF-5.			
DR	InterPro: IPR000478; TNF_family.			
DR	Pfam: PF00229; TNF_1.			
DR	PRODOM: PD008600; TNF_5; 1.			
DR	SMART: SM00207; TNF_1.			
DR	PROSITE: PS50049; TNF_2; 1.			
SO	SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;			

Query Match 97.7%; Score 1525.5; DB 11; Length 313;
Best Local Similarity 98.6%; Pred. No. 1.5e-132;


```
ID 09BDM3 PRELIMINARY: PRT: 261 AA.
AC 09BDM3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Aotus trivirgatus (Night monkey) (Douroucoull).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Boslik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344860; AAK37542.1; -
DR HSSP; P29965; 1ALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 261 AA; 29357 MW; 85E1588B507901B5 CRC64;

Query Match 11.6%; Score 180.5; DB 6; Length 261;
Best Local Similarity 26.3%; Pred. No. 1.4e-08;
Matches 77; Conservative 50; Mismatches 115; Indels 51; Gaps 16;

OY 10 PAPSAPAPAPASRSRFLALLGIGGVCSIALF-LYRAQMDPRKSEDSTHCFYR 68
DB 8 PAPSAPAPAPASRSRFLALLGIGGVCSIALF-LYRAQMDPRKSEDSTHCFYR 68
OY 69 ILRLHENDLQDSTLESSEDTLPDS-----CRMQAQAGAVQKELQHVQPRSGAPAM 123
DB 58 --NLHEDVPM-KTIQRKNTGERSLSLNCETIKSDFEGFV-KDIM-----LNKEEK 106
OY 124 MEGSLDVAQGRKPEAPFAHLITNAISPSGSHKVTLSWYHGRMAKISN--MTLSNG 181
DB 107 KENSE--EMQKGDQNPQIAAHV-----ISEASSKTSVQLMAEKGYTSMNLVTLENG 138
OY 182 K-LRVNODGFYLLANICF-RHNETSGSVPTDYQLMAYVYVTKSIKIPSSHN--LMKGS 237
DB 159 KQLVKKGGLYTYAQTFFCSNREASSQAP-----FLASLCLKPRNFERILLRAAN 210
OY 238 TKMNSGSEFFHYSIYNGGFKLKAGEEISIOVSNPSLLDPDDATYEGAFKV 290
DB 211 TH--SSAKPCQGSINHLGIFELDPGASVFNVTDPQSVSHGTGFTSFGLLKL 261

RESULT 11
ID 09MYL6 PRELIMINARY: PRT: 280 AA.
AC 09MYL6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FAS LIGAND.
OS Macaca nemestrina (Pig-tailed macaque).
OS Macaca fascicularis (Crap eating macaque) (Cynomolus monkey), and
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545, 9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Pig-called monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLUS MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Cynomolus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=RHEBUS MONKEY;
RA Kiril Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BAA90296.1; -
DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035139; BAA90295.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF_1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.5%; Score 179; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 2.1e-08;
Matches 67; Conservative 45; Mismatches 102; Indels 92; Gaps 10;

OY 3 PHEGRLPAPAPAP--APPAPASRS-----MFLALLGIGGVCSIALF 46
DB 49 PRPPRLPRPPRLPLPLPLPKKRNHSTGLVMFPMVALVALGGLG-----MF 101
OY 47 LYRAQMDPRKSEDSTHCFYRLRLHENDLQDSTLESSEDTLPDSCRMQAQAGAVQK 106
DB 102 QLEHLD-----KELALELRETSQKHTA-----SLEK 128
OY 107 ELQHIYQPRFGSAPAMMEGSLDVAQGRKPEAPFAHLIT--INAAISPSGSHKVTLSW 164
DB 129 QIQHPRPPE-----KKQQRVAVHLTGKPNRSMP-----LEW 161
OY 165 YHGRMAKISNMTLSNGKLRVNODGFYLLANICFRHNETSGSVPTDYQLMAYVYVTKSI 224
DB 162 EDTYGVILLGVKKYKGGVAVNETGLTFYYSKVYRGGSCIN-----LPLSHKYYMNS 215
OY 225 KIPSSHNLKMGSGSTKMWGNSSEFFHYSIYNGGFKLKAGEEISIOVSNPSLLDPDDATY 284
DB 216 KYPQDLVME--GKMMSYCTTGQMAHSSYLGAVENTLSADHLVYVSELVNFEESTF 274
OY 285 FGAFKV 290
DB 275 FGLYKL 280

RESULT 12
ID 09BDM5 PRELIMINARY: PRT: 280 AA.
AC 09BDM5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545, 9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
```

OC Cercopithecinae: Macaca.
 NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 "Cloning, sequencing, and co-stimulatory molecules."
 RT Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344856; AAK37539.1; .
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR002965; P-rich_extensn.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF_1; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 SO SEQUENCE 280 AA; 31377 MW; 729EA61436F2D398 CRC64;

Query Match 11.3%; Score 177; DB 6; Length 280;
 Best Local Similarity 21.9%; Pred. No. 3.1e-08;
 Matches 67; Conservative 44; Mismatches 103; Indels 92; Gaps 10;

QY 3 PHEGRLPAPAPAP--APPAPASRS-----MFALLGLGIGVCSIALF 46
 DB 49 PPPPLPPPPPLPLPLPLPKKGNHSTGLCLVFMFVALVALGIGL-----MF 101
 QY 47 LYFRAQMDPNRISDSHCFYRLRLHENADLDSTLESDTLPDSCRMAQAFGAVOK 106
 DB 102 QLFHLQ-----KELALRETSQKHTA-----SSLEK 128
 QY 107 ELQHTVGPFRSGAPAMEGSWLDVAQGRKPAOPFAHLT--INAATPSGSHKVTLSW 164
 DB 129 QIGHPSPPE-----KKEQKVAHLTGKPNRSMF-----LEW 161
 QY 165 YHNRGAKISNMTLSNGKRLVNDGFFLYLANICFRHHTSGSVPTDYLQLMVYVYKTSI 224
 DB 162 EDTYGIYVLSGVKKYKGGVINEGLTFYYSKYVFRGSCSTN-----LPLSHKTYMRNS 215
 QY 225 KIPSSHNLKMGSGTKNMSGNSEFHFYSINVGGFKLAGEEISIOVSNPSLLDPDODATY 284
 DB 216 KYPDOLVME--GKMMSYCTTGQMAHSSYLGAVALNSTADHLVYVNSLSLVNEESOTF 274
 QY 285 FGAFKV 290
 DB 275 FGLYKL 280

RESULT 13
 Q9BDN1 PRELIMINARY; PRT; 280 AA.
 ID Q9BDN1
 AC Q9BDN1; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CD95L PROTEIN.
 GN CD95L.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;

RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344847; AAK37606.1; .
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR002965; P-rich_extensn.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF_1; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 SO SEQUENCE 280 AA; 31407 MW; 729EA60067BD398 CRC64;

Query Match 11.2%; Score 175; DB 6; Length 280;
 Best Local Similarity 21.9%; Pred. No. 4.8e-08;
 Matches 67; Conservative 44; Mismatches 103; Indels 92; Gaps 10;

QY 3 PHEGRLPAPAPAP--APPAPASRS-----MFALLGLGIGVCSIALF 46
 DB 49 PPPPLPPPPPLPLPLPLPKKGNHSTGLCLVFMFVALVALGIGL-----MF 101
 QY 47 LYFRAQMDPNRISDSHCFYRLRLHENADLDSTLESDTLPDSCRMAQAFGAVOK 106
 DB 102 QLFHLQ-----KELALRETSQKHTA-----SSLEK 128
 QY 107 ELQHTVGPFRSGAPAMEGSWLDVAQGRKPAOPFAHLT--INAATPSGSHKVTLSW 164
 DB 129 QIGHPSPPE-----KKEQKVAHLTGKPNRSMF-----LEW 161
 QY 165 YHNRGAKISNMTLSNGKRLVNDGFFLYLANICFRHHTSGSVPTDYLQLMVYVYKTSI 224
 DB 162 EDTYGIYVLSGVKKYKGGVINEGLTFYYSKYVFRGSCSTN-----LPLSHKTYMRNS 215
 QY 225 KIPSSHNLKMGSGTKNMSGNSEFHFYSINVGGFKLAGEEISIOVSNPSLLDPDODATY 284
 DB 216 KYPDOLVME--GKMMSYCTTGQMAHSSYLGAVALNSTADHLVYVNSLSLVNEESOTF 274
 QY 285 FGAFKV 290
 DB 275 FGLYKL 280

RESULT 14
 Q9BDC7 PRELIMINARY; PRT; 261 AA.
 ID Q9BDC7
 AC Q9BDC7; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CD154 PROTEIN.
 GN Macaca mulatta (Rhesus macaque), and
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544; 9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP SPECIES=M.mulatta, and C.torquatus atys;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 0:0-0(2001).

DR EMBL: AF344859; AAK37541.1; -
 DR EMBL: AF344841; AAK37600.1; -
 DR HSP; P29965; 1ALV.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR004478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 FT VARIANT 60 60 H -> Q.
 FT VARIANT 204 204 I -> V.
 FT VARIANT 206 206 L -> P.
 FT VARIANT 215 215 A -> T.
 SO SEQUENCE 261 AA; 29366 MW; AA2E0F11C0F28ABB CRC64;

Query Match 11.2%; Score 174.5; DB 6; Length 261;
 Best Local Similarity 25.0%; Pred. No. 4.8e-08;
 Matches 73; Conservative 51; Mismatches 119; Indels 49; Gaps 15;

QY 10 PAPSADPAPPPAASRSMFLALGLIGOVCSIALFLYFRQMDPNRISDSTHCFYRI 69
 DB 8 PSPRSATGIPVPMKIFMYLITFL-ITQMIGSALFAVYLHRRLD--KIEDR----- 57
 QY 70 LRLEHNAADLDSTLESDTLPPDS-----CRMKAFQCAVOKELQHIIVGQRFSGAPAM 124
 DB 58 -NIHEDFVPM-KIQRCNTERSLSLNCEIKSQFEGFV-KDIM-----LNKEKKK 107
 QY 125 EGSMLDVAGRGPEAOPFAHLTINNASIPSGSHKYTLSSWYHDSGMKISN--MTLSNGK 182
 DB 108 ENSF--EMQKGDQNPQIAHV-----ISEASKTTSVLQMAEKGYTMSNNLVTLENGK 159
 QY 183 -LRVNODGFYLYANICF-RHNETSGSVPTDYQLQMLVYVVKTSIKIPSSH--LMKGSST 238
 DB 160 QLTVKRGGLYLYAQTVECSNREASSQAP-----FIASLCKSPGRFERILLRAANT 211
 QY 239 KMWSCNSEFHFYSINVGFFKLRAGEEISIOVSNPLDPPDQATYFCAFKV 290
 DB 212 H--SSAKPCGQSIHLGCVFELQPGASVFNVTDPQVSHGTGFTSGLKL 261

RESULT 15
 Q95N10 PRELIMINARY; PRT; 282 AA.
 AC Q95N10;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PAS LIGAND.
 GN PASL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhu N., Young Y.;
 RT "Molecular cloning and characterization of porcine Pas ligand cDNA";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY033634; AAK56449.1; -
 SO SEQUENCE 282 AA; 31752 MW; F391212406AE1E7D CRC64;

Query Match 11.1%; Score 173; DB 6; Length 282;
 Best Local Similarity 21.6%; Pred. No. 7.4e-08;
 Matches 66; Conservative 45; Mismatches 102; Indels 92; Gaps 10;

QY 3 PHEGRLPAPSDAPAPPPAASNS-----MFLALGLIGOVCSIALFL 47
 DB 53 PPPPLLPSPRLP-PLPPSLKKRKHNAAGLCILVFFWLVALVGLGLG-----MFQ 104
 QY 48 YFRAQMDPNRISDSTHCFYRLRLHENAADLDSTLESDTLPPDSGRMKAFQCAVOK 107

DB 105 LFHLQKE-----LTELRESASQRHT-----ESSLEKQ 131
 QY 108 LOHIIVGQRFSGAPAMMEGSMVDVAGRGKPEAOPFAHLT--INNASIPSGSHKYTLSSWY 165
 DB 132 IGHPLPSE-----KKELRKVAHLTGKPNRSRIP-----LEWE 164
 QY 166 HDRCAKISNMTLSNGKLRVNODGFYLYANICFRHNETSGSVPTDYQLQMLVYVVKTSIK 225
 DB 165 DTYGIALVSGVYKMGSLIVNDTGLYFYSKYVFRGOYCNQ-----PLSHKYVTRNSR 218
 QY 226 IPPSHNLMKGGSTKMWSCNSEFHFYSINVGFFKLRAGEEISIOVSNPLDPPDQATYF 285
 DB 219 YPQDLVLMG-GKMMNYCTTGQMMARSSYLGAVFNLTSADHLVYVNSLSLVNFEESKTF 277
 QY 286 GAFKV 290
 DB 278 GLYKL 282

Search completed: July 8, 2002, 19:52:38
 Job time: 12582 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 23:50:08 ; Search time 4715.96 Seconds
(without alignments)
4233.267 Million cell updates/sec

Title: US-09-865-363-12

Perfect score: 954
Sequence: 1 ATCCGCCGCCGACAGAGA.....AAGTTCGAGATATAGATTGA 954

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pl:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	954	100.0	954	6	AR156434	AR156434 Sequence
2	954	100.0	954	6	AR164148	AR164148 Sequence
3	954	100.0	954	6	AX147989	AX147989 Sequence
4	954	100.0	1034	9	AB064269	AB064269 Homo sapi
5	954	100.0	2201	9	AF019047	AF019047 Homo sapi
6	954	100.0	2271	9	AF053712	AF053712 Homo sapi
7	858	89.9	911	9	AB061227	AB061227 Homo sapi
8	822.2	86.2	972	9	AB064270	AB064270 Homo sapi
9	790	82.8	818	9	AB064268	AB064268 Homo sapi
10	739	77.5	930	9	AB037599	AB037599 Homo sapi
11	733.2	76.9	2390	6	AX201362	AX201362 Sequence
12	675.4	70.8	1823	9	AF013171	AF013171 Homo sapi
13	666.2	69.8	2225	10	AF019048	AF019048 Mus muscu
14	666.2	69.8	951	6	E34350	E34350 DNA and pro
15	666.2	69.8	951	6	E36388	E36388 Novel prote
16	666.2	69.8	951	10	AB008426	AB008426 Mus muscu
17	666.2	69.8	951	10	AB036798	AB036798 Mus muscu
18	666.2	69.8	2191	6	AR157058	AR157058 Sequence
19	666.2	69.8	2191	6	AX140162	AX140162 Sequence
20	666.2	69.8	2295	6	AR062119	AR062119 Sequence
21	666.2	69.8	2237	10	AF053713	AF053713 Mus muscu
22	666.2	69.8	2237	10	AF013170	AF013170 Mus muscu
23	663	69.5	1630	6	AR156433	AR156433 Sequence
24	615	64.5	1630	6	AR164147	AR164147 Sequence
25	615	64.5	1630	6	AX147987	AX147987 Sequence
26	615	64.5	1630	6	AB032771	AB032771 Mus muscu
27	591.8	62.0	864	10	AB032772	AB032772 Mus muscu
28	511.6	53.6	754	10	AB022036S4	AB022036 Mus muscu
29	425	44.5	113451	2	AC023297	AC023297 Homo sapi
30	425	44.5	200724	9	AL139382	AL139382 Human DNA
31	365.6	38.3	522	6	AX232589	AX232589 Sequence
32	327	34.3	123551	2	AC094149	AC094149 Rattus no
33	325.4	34.1	2029	6	E34349	E34349 DNA and pro
34	325.4	34.1	2029	10	AB022036S4	AB022036 Mus muscu
35	153	16.0	764	10	AB022036S1	AB022036 Mus muscu
36	151.4	15.9	2026	6	E34346	E34346 DNA and pro
37	126.6	13.3	123551	2	AC094149	AC094149 Rattus no
38	125.4	13.1	161835	2	AC104794	AC104794 Homo sapi
39	125.4	13.1	190748	9	AC010969	AC010969 Homo sapi
40	124	13.0	809	10	AF425669	AF425669 Rattus no
41	114.2	12.0	468	6	E34347	E34347 DNA and pro
42	114.2	12.0	468	10	AB022036S2	AB022037 Mus muscu
43	104.2	7.9	113451	2	AC023297	AC023297 Homo sapi
44	71	7.4	157943	2	AC016938	AC016938 Homo sapi
45	71	7.4	167810	9	AC007051	AC007051 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AR156434 954 bp DNA
DEFINITION Sequence 12 from patent US 6242213.
ACCESSION AR156434
VERSION AR156434.1 GI:15125138
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 954)
AUTHORS Anderson,D.M.
TITLE Isolated DNA molecules encoding RANK-L
JOURNAL Patent: US 6242213-A 12 05-JUN-2001;
FEATURES
source location/Qualifiers
1..954
BASE COUNT 255 a 239 c 227 g 233 t
ORIGIN

Query Match 100.0%; Score 954; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 5.6e-188;

Matches	954: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
Oy	1	ATGGCGCGCGCCACACAGACTACACCAGTACCTGCGTGTGAGGAGATGGCGC	60		
Db	1	ATGGCGCGCGCCACACAGACTACACCAGTACCTGCGTGTGAGGAGATGGCGC	60		
Oy	61	GGCCCCGAGAGCCCCGACAGAGGGCCCCCTGCAGCCCCCGCGCTGTGGCGGCACAG	120		
Db	61	GGCCCCGAGAGCCCCGACAGAGGGCCCCCTGCAGCCCCCGCGCTGTGGCGGCACAG	120		
Oy	121	CCCCCGCGCGCTCCCGCTCATGTTCGTGGCCCTCCCTGGGGCTGGGGCTGGGCAAGTT	180		
Db	121	CCCCCGCGCGCTCCCGCTCATGTTCGTGGCCCTCCCTGGGGCTGGGGCTGGGCAAGTT	180		
Oy	181	GTCGTACAGCGTGGCCCTGCTTCTTATTTTCAGAGCGAGATGATCTCTAATAGATATCA	240		
Db	181	GTCGTACAGCGTGGCCCTGCTTCTTATTTTCAGAGCGAGATGATCTCTAATAGATATCA	240		
Oy	241	GAAAGTGGCACTGCACCTGATTTATAGAAATTTGAGACTCCCTGAAATGCAATTTTCAA	300		
Db	241	GAAAGTGGCACTGCACCTGATTTATAGAAATTTGAGACTCCCTGAAATGCAATTTTCAA	300		
Oy	301	GACACAACTCTGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGAGAAATTTAA	360		
Db	301	GACACAACTCTGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGAGAAATTTAA	360		
Oy	361	CAGGCTTTCAAAGAGCTGTGCATAAAGAAATTAACAATATACGTGTGATCTCAGACATAC	420		
Db	361	CAGGCTTTCAAAGAGCTGTGCATAAAGAAATTAACAATATACGTGTGATCTCAGACATAC	420		
Oy	421	AGAGCAGAGAAAGCAGTGGTGGATGGCTCATGGTTAGATCTGGCCAAAGAGGAGCAAGCTT	480		
Db	421	AGAGCAGAGAAAGCAGTGGTGGATGGCTCATGGTTAGATCTGGCCAAAGAGGAGCAAGCTT	480		
Oy	481	GAACTCAGCCCTTTTGCTCATCTACTATTATATGCAACCGACATCCATCTGGTTCCAT	540		
Db	481	GAACTCAGCCCTTTTGCTCATCTACTATTATATGCAACCGACATCCATCTGGTTCCAT	540		
Oy	541	AAAGTGAAGCTGCTGCTTTGGTGCATATGAGGAGGAGGTTGGCCAAAGATCCCAATGACT	600		
Db	541	AAAGTGAAGCTGCTGCTTTGGTGCATATGAGGAGGAGGTTGGCCAAAGATCCCAATGACT	600		
Oy	601	TTTACCAATGAGAAACTAATAGTATATCAGATGAGCTTTTATACCTGTATGCCAATTT	660		
Db	601	TTTACCAATGAGAAACTAATAGTATATCAGATGAGCTTTTATACCTGTATGCCAATTT	660		
Oy	661	TGCTTTCGACATCATGAAGAACTCAGAGAGCCAGTATAGAGATATCTCACTAATGCTG	720		
Db	661	TGCTTTCGACATCATGAAGAACTCAGAGAGCCAGTATAGAGATATCTCACTAATGCTG	720		
Oy	721	TACGTCACATAAACAGATCAAAATCCCAAGTTCATACCTGTATGAAAGAGAGAAC	780		
Db	721	TACGTCACATAAACAGATCAAAATCCCAAGTTCATACCTGTATGAAAGAGAGAAC	780		
Oy	781	ACCAAGTATGGTCAGGGGAATCTGAATTCATTTTATTCATAAGGTGGTGGATTT	840		
Db	781	ACCAAGTATGGTCAGGGGAATCTGAATTCATTTTATTCATAAGGTGGTGGATTT	840		
Oy	841	TTTAAATTAAGTTCAGGTCTGGAGAGGAAATCAGCATGAGGTCTCCAAACCTCTTACTGAT	900		
Db	841	TTTAAATTAAGTTCAGGTCTGGAGAGGAAATCAGCATGAGGTCTCCAAACCTCTTACTGAT	900		
Oy	901	CCGGATCAGAGATGCAAATATCTTTGGGGCTTTTAAAGTTCGAGATATGATTTGA	954		
Db	901	CCGGATCAGAGATGCAAATATCTTTGGGGCTTTTAAAGTTCGAGATATGATTTGA	954		
RESULT 2					
LOCUS	AR164148	954 bp	DNA	linear	PAT 17-OCT-2001
DEFINITION	Sequence 12 from patent US 6271349.				
ACCESSION	AR164148				
VERSION	AR164148.1 GI:16235114				

KEYWORDS	.	Unknown.			
SOURCE		Unknown.			
ORGANISM		Unclassified.			
REFERENCE	1	(bases 1 to 954)			
AUTHORS		Dougall, W. C. and Galibert, L.			
TITLE		Receptor activator of NF- κ B			
JOURNAL		Patent: US 6271349-A 12 07-AUG-2001;			
FEATURES		Location/Qualifiers			
	1..954				
source		/organism="unknown"			
BASE COUNT	255	a	239	c	227
ORIGIN					g
					233
					t

Query Match	100.0%	Score 954:	DB 6:	Length 954:
Best Local Similarity	100.0%	Pred. No. 5.6e-188:		
Matches 954:	Conservative	0:	Mismatches 0:	Indels 0:
QY	1	ATGCGCGCGGCGCAGAGACTACACCAAGTACCTGCGCTGCGAGAGATGCGCGC	60	
Db	1	ATGCGCGCGCGCAGAGACTACACCAAGTACCTGCGCTGCGAGAGATGCGCGC	60	
QY	61	GGCGCCGGAGCGCCCGCACAGAGGCGCCCTGCAAGCGCCCGCGCTGCGCCACACAG	120	
Db	61	GGCGCCGGAGCGCCCGCACAGAGGCGCCCTGCAAGCGCCCGCGCTGCGCCACACAG	120	
QY	121	CCCCCGCGCGCCCGCGTCATGTTTCGCGGCCCTCTGGGGCTGGGGCTGGGCACAGTT	180	
Db	121	CCCCCGCGCGCCCGCGTCATGTTTCGCGGCCCTCTGGGGCTGGGGCTGGGCACAGTT	180	
QY	181	GTCGTCAGCGTCGCGCCCTGTTCTTATTTTCAGAGCGCAGATGGATCTTATAGATATCA	240	
Db	181	GTCGTCAGCGTCGCGCCCTGTTCTTATTTTCAGAGCGCAGATGGATCTTATAGATATCA	240	
QY	241	GAAGATGGCACTACGTCAGCTTATTAAGTTTGAAGTCCATGAAGAAATCAGATTTTCAA	300	
Db	241	GAAGATGGCACTACGTCAGCTTATTAAGTTTGAAGTCCATGAAGAAATCAGATTTTCAA	300	
QY	301	GACACAACTCTGGAGAGTCAGATACAAAATTATACCTGATTCATGTAGAGATTTAA	360	
Db	301	GACACAACTCTGGAGAGTCAGATACAAAATTATACCTGATTCATGTAGAGAAATTA	360	
QY	361	CAGGCTTTCAAGGACTGTGCAAAAGGAATTCAACATATCGTTGGATCACAGCAATC	420	
Db	361	CAGGCTTTTAAAGAGGTGTGCAAAAGGAATTCAACATATCGTTGGATCACAGCAATC	420	
QY	421	AGAGCAGAGAAACGATGTGTGATGGCTCATGTTAGATCGGCCAAGAGACAGACTT	480	
Db	421	AGAGCAGAGAAACGATGTGTGATGGCTCATGTTAGATCGGCCAAGAGACAGACTT	480	
QY	481	GAAGCTAGGCTTTGGTCATCTCAGTATTAATGCGCAGACATCCCATCTGGTTCCCAT	540	
Db	481	GAAGCTAGGCTTTGGTCATCTCAGTATTAATGCGCAGACATCCCATCTGGTTCCCAT	540	
QY	541	AAAGTGAATCTGTCTCTTGGTACCATGATCGGAGTTGGGCCAAGATCTTCAACATGACT	600	
Db	541	AAAGTGAATCTGTCTCTTGGTACCATGATCGGAGTTGGGCCAAGATCTTCAACATGACT	600	
QY	601	TTTATGCAATGAAGAAACTAATAGTTAATCAGAGATGGCTTTTATTAACCTGTAATGCGCAACATT	660	
Db	601	TTTATGCAATGAAGAAACTAATAGTTAATCAGAGATGGCTTTTATTAACCTGTAATGCGCAACATT	660	
QY	661	TGCTTTGACATCATGAAACTTCAGAGACCTAGCTACAGATCTTCACTAATATGCTG	720	
Db	661	TGCTTTGACATCATGAAACTTCAGAGACCTAGCTACAGATCTTCACTAATATGCTG	720	
QY	721	TACGTCACATAAACACAGATCAAAATTCCCAAAGTTTCATACCTGATGAAGAGGAGAGC	780	
Db	721	TACGTCACATAAACACAGATCAAAATTCCCAAAGTTTCATACCTGATGAAGAGGAGAGC	780	
QY	781	ACCAAGATTGCTCAGGAATTTCGAATTCATTTTATTCATAAAGCTTGGTGAATTT	840	


```
Db 781 ACCAACTATTGTCAGGAAATTCGAATTCATTTTATTCATMAAACCTGTGGATTT 840
Oy 841 TTTAACTAGGCTCTGAGAGAGAAATCAGATCGAGGCTCCAAOCCCTCTTACGAT 900
Db 841 TTTAACTAGGCTCTGAGAGAGAAATCAGATCGAGGCTCCAAOCCCTCTTACGAT 900
Oy 901 CCGGATCAGAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTTGA 954
Db 901 CCGGATCAGAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTTGA 954

RESULT 3
AX147989
LOCUS AX147989 954 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 12 from Patent WO0136637.
ACCESSION AX147989
VERSION AX147989.1 GI:14346964
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Anderson D.M. and Hughes A.E.
TITLE Receptor activator of nf-kappa b
JOURNAL Patent: WO 0136637-A 12 25-MAY-2001;
Immunex Corporation (US)
FEATURES
source
1..954
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..954
/note="unnamed protein product"
/codon_start=1
/db_xref="GI:14346965"
/translating="MRRASRYTYKYLNGSEMGCGPCAPHEGPHAPPPAPHPAPPA
SRKRFVALLGLGQVCSVALFFYFAOMDPNISI SDGTHCIRILRLHENDFODT
TLESQDRLIPDSORIKQAFQAVOKELIVGSHIRAKMAVDSDMLAKRSKL
EAPFAHLITNADIPSGSHKVSLSWYHBRGMKISNMGFSNKLIVNDGFYLYA
NICPHHETSGDLATEYLQMLVYVTKYSIKPSHITLMKSGSTKYSWGNSDFPHYSIN
VGFFKLRSGEISIEVSNPSILDPDODATYFGAFKRYDID"

BASE COUNT 255 a 239 c 227 g 233 t
ORIGIN
```

```
Query Match 100.0%; Score 954; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 5.6e-188;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 ATGGCCCGCCGACAGACTACACCAAGTACCTGCTGCTCGAGAGATGGCGGC 60
Db 1 ATGGCCCGCCGACAGACTACACCAAGTACCTGCTGCTCGAGAGATGGCGGC 60
Oy 61 GGCCCGGAGCCGCGACAGAGGCGCCCTGACGCGCCCGCCGCTGCGCCGACAC 120
Db 61 GGCCCGGAGCCGCGACAGAGGCGCCCTGACGCGCCCGCCGCTGCGCCGACAC 120
Oy 121 CCCCCCGCGGCTCCCGCTCATGTGTGCGCCCTCTGCGGCTGCGGCTGCGCAG 180
Db 121 CCCCCCGCGGCTCCCGCTCATGTGTGCGCCCTCTGCGGCTGCGGCTGCGCAG 180
Oy 181 GTTCGACGCGGCGGCTCTTCTATTTTCAGACGCGAGATGATCTTAATAAGAT 240
Db 181 GTTCGACGCGGCGGCTCTTCTATTTTCAGACGCGAGATGATCTTAATAAGAT 240
Oy 241 GAAGATGCACTCACTGATTTATAGAAATTTGAGACCTCAATGAAGATTTTCA 300
Db 241 GAAGATGCACTCACTGATTTATAGAAATTTGAGACCTCAATGAAGATTTTCA 300
Oy 301 GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATCTAGAGAAATTA 360
Db 301 GACACAACTCTGAGAGTCAAGATACAAATTAATACCTGATCTAGAGAAATTA 360
```

```
Oy 361 CAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACATATCGTTGATCACAGCATC 420
Db 361 CAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACATATCGTTGATCACAGCATC 420
Oy 421 AGACAGAGAAAGGATGGTGGATGCGTCAATGATCTGCGCAAGAGAGCAAGCT 480
Db 421 AGACAGAGAAAGGATGGTGGATGCGTCAATGATCTGCGCAAGAGAGCAAGCT 480
Oy 481 GAAGCTGACCTTTTGTCTCATCTCATATTAATGACCAACGATCCATCGTTCCAT 540
Db 481 GAAGCTGACCTTTTGTCTCATCTCATATTAATGACCAACGATCCATCGTTCCAT 540
Oy 541 AAGTGAATCTGTCTCTCTGTTGATACCATGATCGGGGTTGGCCAAAGATCCACATGAT 600
Db 541 AAGTGAATCTGTCTCTCTGTTGATACCATGATCGGGGTTGGCCAAAGATCCACATGAT 600
Oy 601 TTTAGCAATGGAAGAACTAATGTTAATCAGATGCGCTTTTATTCGTATGCCAAT 660
Db 601 TTTAGCAATGGAAGAACTAATGTTAATCAGATGCGCTTTTATTCGTATGCCAAT 660
Oy 661 TGTCTTGACATCATGAAGATTCAGAGACCTAGCTACAGATCTTCAACTAATG 720
Db 661 TGTCTTGACATCATGAAGATTCAGAGACCTAGCTACAGATCTTCAACTAATG 720
Oy 721 TAGCTCACTAAACACGATCAAAATCCCAAGTTCTCATACCCGATGAAAGAGAAC 780
Db 721 TAGCTCACTAAACACGATCAAAATCCCAAGTTCTCATACCCGATGAAAGAGAAC 780
Oy 781 ACCAAGTATTGCTGAGGAAATTCGAATTCATTTTATTCATTAAGCTTGGTGAT 840
Db 781 ACCAAGTATTGCTGAGGAAATTCGAATTCATTTTATTCATTAAGCTTGGTGAT 840
Oy 841 TTTAAGTTAGGCTGTCAGAGAGAAATAGCATGAGGCTTCCAAOCCCTCTTAC 900
Db 841 TTTAAGTTAGGCTGTCAGAGAGAAATAGCATGAGGCTTCCAAOCCCTCTTAC 900
Oy 901 CCGGATCAGAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTTGA 954
Db 901 CCGGATCAGAGATGCAACATCTTTGGGCTTTTAAAGTTGAGATATGATTTGA 954

RESULT 4
AB064269
LOCUS AB064269 1034 bp mRNA linear PRI 26-DEC-2001
DEFINITION Homo sapiens hRANKL 1 mRNA for receptor activator of nuclear factor
ACCESSION AB064269
VERSION AB064269.1 GI:18143618
KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ikeda,T., Kuroyama,H. and Hirokawa,K.
TITLE Determination of human RANKL isoforms
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1034)
AUTHORS Ikeda,T. and Kuroyama,H.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental
University, Department of Pathology and Immunology, Graduate
School, Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan
(E-mail:tohru.plh2@med.tmd.ac.jp, Tel:81-3-5803-5176,
Fax:81-3-5803-0123)
FEATURES
source
1..1034
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
81..1034
/gene="hRANKL 1"
81..1034
CDS
```

```
/gene="hRANKL 1"
/codon_start=1
/product="receptor activator of nuclear factor kappa B
ligand 1"
/db_xref="GI:18143619"
/translation="MRRASRDYTKYLRSPEMGSGPAPHEGPIAHPPAPHPQPPA
SRMFAVLGLGQVVCVALFFFAQDPRISEDGHCIRILRLHENDPDDT
TLESODTKLIPDSGRIRKQAFQAGVOKELQIHVSGHIRAEKAWDGSWLAKRSKL
EAOPFAHLITINADIPSGSHKVSLSWYHHRGNAKISNMTFSGKLIVNDGFYLYLA
NICEFHETSGDLATEYLQIMVYVTKSIKIPSSHTLMKGSSTRKYSNSEFHYYSIN
VGGEFKLRSGEIEISVSNPSILDDPDATYFAGFKVDDID"
BASE COUNT      275 a      257 c      265 g      237 t
ORIGIN

Query Match      100.0%; Score 954; DB 9; Length 1034;
Best Local Similarity 100.0%; Pred. No. 5,7e-188;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
|||||
Db      861 ACCAGATTTGGTCAGGAAATTCGAATCTTTTATTCATTAACGTGGTGATTT 920
QY      841 TTTAAGTTACGGTCTGAGAGGAATACAGATGAGGTCTCCAAACCCCTTACGAT 900
      |||||||
Db      921 TTTAAGTTACGGTCTGAGAGGAATACAGATGAGGTCTCCAAACCCCTTACGAT 980
QY      901 CCGATCAGATGCACATCTTTGGGCTTTTAAAGTTGAGATATAGATTGA 954
      |||||||
Db      981 CCGATCAGATGCACATCTTTGGGCTTTTAAAGTTGAGATATAGATTGA 1034

RESULT      5
AF019047      2201 bp      mRNA      linear      PRI 22-NOV-1997
LOCUS      AF019047
DEFINITION      Homo sapiens receptor activator of nuclear factor kappa B ligand
ACCESSION      (RANKL) mRNA, complete cds.
VERSION      AF019047
KEYWORDS      AF019047.1 GI:2612921
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 2201)
      Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
      Rometsko,M.E., Roux,E.R., Teepe,M.C., Dubose,R.F., Cosman,D. and
      Galibert,L.
      A homologue of the TNF receptor and its ligand enhance T-cell
      growth and dendritic-cell function
      Nature 390 (656), 175-179 (1997)
      98032977
      2 (bases 1 to 2201)
      Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
      Cosman,D., Dubose,R. and Galibert,L.
      Direct Submission
      Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
      University St., Seattle, WA 98101, USA
      Location/Qualifiers
      1..2201
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="13"
      /map="13q14"
      1..2201
      /gene="RANKL"
      129..1082
      /note="receptor activator of nuclear factor kappa B
      ligand"
      /codon_start=1
      /product="RANKL"
      /protein_id="AAB86811.1"
      /db_xref="GI:2612922"
      /translation="MRRASRDYTKYLRSPEMGSGPAPHEGPIAHPPAPHPQPPA
      SRMFAVLGLGQVVCVALFFFAQDPRISEDGHCIRILRLHENDPDDT
      TLESODTKLIPDSGRIRKQAFQAGVOKELQIHVSGHIRAEKAWDGSWLAKRSKL
      EAOPFAHLITINADIPSGSHKVSLSWYHHRGNAKISNMTFSGKLIVNDGFYLYLA
      NICEFHETSGDLATEYLQIMVYVTKSIKIPSSHTLMKGSSTRKYSNSEFHYYSIN
      VGGEFKLRSGEIEISVSNPSILDDPDATYFAGFKVDDID"
BASE COUNT      658 a      429 c      497 g      617 t
ORIGIN

Query Match      100.0%; Score 954; DB 9; Length 2201;
Best Local Similarity 100.0%; Pred. No. 6,1e-188;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Db 189 GGGCCCGGAGCCCGGACAGAGGGCCCGGCGACGCGCCGCGCGCGCGGACAG 248
Oy 121 CCCCCCGCCCGCTCCCGCTCATGTTTCGCGCCCTCTGGGGCTGGGGCCAGGTT 180
Db 249 CCCCCCGCCCGCTCCCGCTCATGTTTCGCGCCCTCTGGGGCTGGGGCCAGGTT 308
Oy 181 GTCGTGAGCGTGGCCCTGTCTTCTTATTTTCAGAGCGCAGAGGATCTTAATGAATCA 240
Db 309 GTCGTGAGCGTGGCCCTGTCTTCTTATTTTCAGAGCGCAGAGGATCTTAATGAATCA 368
Oy 241 GAAGATGGCACTCACTGCATTTATGAATTTTGAAGTCCAGTAAATGCAATTTTCAA 300
Db 369 GAAGATGGCACTCACTGCATTTATGAATTTTGAAGTCCAGTAAATGCAATTTTCAA 428
Oy 301 GACACAACCTGAGAGTCAACATCAAAATTAATACCTGATTCATGTAGAGAAATTA 360
Db 429 GACACAACCTGAGAGTCAACATCAAAATTAATACCTGATTCATGTAGAGAAATTA 488
Oy 361 CAGGCTTTCAAGAGAGTGTGCAAAAGAAATTAACAATTCGTTGATCACAGCATC 420
Db 489 CAGGCTTTCAAGAGAGTGTGCAAAAGAAATTAACAATTCGTTGATCACAGCATC 548
Oy 421 AGAGCAGAGAAAGCGATGGTGGATGCTCATGTAGATCGGCCAAGAGAGAGAGCTT 480
Db 549 AGAGCAGAGAAAGCGATGGTGGATGCTCATGTAGATCGGCCAAGAGAGAGAGCTT 608
Oy 481 GAGCTCAGCCCTTTTGTCTCATCTCATTAATGCGACGACATCCCATCTGTTCCCAT 540
Db 609 GAGCTCAGCCCTTTTGTCTCATCTCATTAATGCGACGACATCCCATCTGTTCCCAT 668
Oy 541 AAGGTGACTGTCTCTCTTGTGATCATGATGGGGTTGGGCCAAGATCTCCAACATGACT 600
Db 669 AAGGTGACTGTCTCTCTTGTGATCATGATGGGGTTGGGCCAAGATCTCCAACATGACT 728
Oy 601 TTTACCAATGGAAAACTAATAGTTAATCAGAGTGGCTTTTATACCTGATGCCAATC 660
Db 729 TTTACCAATGGAAAACTAATAGTTAATCAGAGTGGCTTTTATACCTGATGCCAATC 788
Oy 661 TGCCTTGCACATCATGAACCTTCAGAGAGCTAGCTACAGAGTATCTTCAATATGCTG 720
Db 789 TGCCTTGCACATCATGAACCTTCAGAGAGCTAGCTACAGAGTATCTTCAATATGCTG 848
Oy 721 TAGCTCACTAAACAGACATCAAAATCCCAAGTCTCATACCTGATGAAAGAGAGAAC 780
Db 849 TAGCTCACTAAACAGACATCAAAATCCCAAGTCTCATACCTGATGAAAGAGAGAAC 908
Oy 781 ACCAAGATTTGGTCAAGGAATTCGAATTCATTTTATTCATAAAGTGGTGGATTT 840
Db 909 ACCAAGATTTGGTCAAGGAATTCGAATTCATTTTATTCATAAACGTTGGTGGATTT 968
Oy 841 TTTAAGTTACCGTCTGGAGAGAAATCAGCATCGAGTCTTCAACCCCTCTTACTGGAT 900
Db 969 TTTAAGTTACCGTCTGGAGAGAAATCAGCATCGAGTCTTCAACCCCTCTTACTGGAT 1028
Oy 901 CCGGATCAGATGCAACATACCTTTGGGGCTTTTAAAGTTGAGATATAGATTGA 954
Db 1029 CCGGATCAGATGCAACATACCTTTGGGGCTTTTAAAGTTGAGATATAGATTGA 1082

```

RESULT 6
AF053712
LOCUS AF053712 2271 bp mRNA linear PRI 09-MAY-1998
DEFINITION Homo sapiens osteoprotegerin ligand mRNA, complete cds.
ACCESSION AF053712
VERSION AF053712.1 GI:3057145
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Chordata: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
REFERENCE 1 (bases 1 to 2271)
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,

Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
 Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
 Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Serni, G., Guo, J.,
 Delaney, J., and Boyle, W.J.
 Osteoprotegerin ligand is a cytokine that regulates osteoclast
 differentiation and activation
 Cell 93 (2), 165-176 (1998)
 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
 One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES
source
 1..2271
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 185..1138
 /function="regulates osteoclast differentiation and
 activation"
 /product="osteoprotegerin ligand"
 /codon_start=1
 /protein_id="AAC39731.1"
 /db_xref="GI:3057146"
 /translation="MRASRDYKYLKRGSEMGPGAPHEGLHAPPAPHPAPPA
 SRMFVALGLGLGVCSVALFEYRAADMDPRISDGHCIYRLRHENADRODT
 TRESODPKLIPDSCKRIKQAFQAGAVOKLEIIVGSOHTRAEKAMVDSGLAKSKL
 EAQPFALITNATDIPSGSHKSLSSWYHNDRAKSNKTFPSKGLIVQDGFYLYA
 NICEFRHETSGDLATERYLQIMYVTKTISKIPSHMLMGSGSTKWSNSERHPFYSIN
 VGGFRKRGSEELISIEVSNPSLIDPDQATYFGAFKVRDID"
BASE COUNT 658 a 462 c 522 g 629 t
ORIGIN

Query Match 100.0% Score 954: DB 9: Length 2271:
 Best Local Similarity 100.0%: Pred. No. 6: 1e-188:
 Matches 954: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

Oy 1 ATGGCGCCGCGCCAGCAGAGACTACCAAGTACCTGGTGGCGGAGAGATGGCGGC 60
Db 185 ATGGCGCCGCGCCAGCAGAGACTACCAAGTACCTGGTGGCGGAGAGATGGCGGC 244
Oy 61 GGGCCGGAGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 245 GGGCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
Oy 121 CCCCCCGCGCCCTCCGCTCATGTTGCGGCCCTCTGGGGCTGGGGCCAGGTT 180
Db 305 CCCCCCGCGCCCTCCGCTCATGTTGCGGCCCTCTGGGGCTGGGGCCAGGTT 364
Oy 181 GTCGTGAGCGTGGCCCTGTCTTCTTATTTTCAGAGCGCAGATGATCTTAATGAATCA 240
Db 365 GTCGTGAGCGTGGCCCTGTCTTCTTATTTTCAGAGCGCAGATGATCTTAATGAATCA 424
Oy 241 GAAGATGGCACTCACTGCATTTTATGAATTTTGAAGTCCAGTAAATGCAATTTTCAA 300
Db 425 GAAGATGGCACTCACTGCATTTTATGAATTTTGAAGTCCAGTAAATGCAATTTTCAA 484
Oy 301 GACACAACCTGAGAGTCAACATCAAAATTAATACCTGATTCATGTAGAGAAATTA 360
Db 485 GACACAACCTGAGAGTCAACATCAAAATTAATACCTGATTCATGTAGAGAAATTA 544
Oy 361 CAGGCTTTCAAGAGAGTGTGCAAAAGAAATTAACAATATGTTGGATTCACAGCATC 420
Db 545 CAGGCTTTCAAGAGAGTGTGCAAAAGAAATTAACAATATGTTGGATTCACAGCATC 604
Oy 421 AGAGCAGAGAAAGCGATGGTGGATGCTCATGTTTATGATCTGGCCAAAGAGAGAGCTT 480
Db 605 AGAGCAGAGAAAGCGATGGTGGATGCTCATGTTTATGATCTGGCCAAAGAGAGAGCTT 664
Oy 481 GAGCTCAGCCCTTTTGTCTCATCTCATTAATGCGACGACATCCCATCTGTTCCCAT 540
Db 665 GAGCTCAGCCCTTTTGTCTCATCTCATTAATGCGACGACATCCCATCTGTTCCCAT 724

```

QY 541 AAGTGAAGTCTGCTCTCTGTGGTACCATGATCGGGGTTGGCCCAAGATCTCCAACTACT 600
|||||
Db 725 AAGTGAAGTCTGCTCTCTGTGGTACCATGATCGGGGTTGGCCCAAGATCTCCAACTACT 784
QY 601 TTATGCAATGGAACAACTAATAGTAAATCAGATGCGCTTTTATATCCGTATGCCAATTT 660
|||||
Db 785 TTATGCAATGGAACAACTAATAGTAAATCAGATGCGCTTTTATATCCGTATGCCAATTT 844
QY 661 TGCCTTGACATCATGAACCTTCAGAGACCTACGATGATCTTCACTCAATGATG 720
|||||
Db 845 TGCCTTGACATCATGAACCTTCAGAGACCTACGATGATCTTCACTCAATGATG 904
QY 721 TACGTCACATAAACACAGATCAAAATCCCAAGTTCATACCTGATGAAGAAGAGAAC 780
|||||
Db 905 TACGTCACATAAACACAGATCAAAATCCCAAGTTCATACCTGATGAAGAAGAGAAC 964
QY 781 ACCAAGTATGTCAGGAATTCGAAATTCATTTTATTCATGAACGATGATGATTT 840
|||||
Db 965 ACCAAGTATGTCAGGAATTCGAAATTCATTTTATTCATGAACGATGATGATTT 1024
QY 841 TTAAAGTACGCTGTGAGAGAGAAATCAGATCGAGTCTCCAAACCCCTCTACTGAT 900
|||||
Db 1025 TTAAAGTACGCTGTGAGAGAGAAATCAGATCGAGTCTCCAAACCCCTCTACTGAT 1084
QY 901 CCGGATCGAGATGCAACATCTTTGGGCTTTTAAAGTTCGAGATATGATTGA 954
|||||
Db 1085 CCGGATCGAGATGCAACATCTTTGGGCTTTTAAAGTTCGAGATATGATTGA 1138

RESULT 7

AB061227 911 bp mRNA linear PRI 03-NOV-2001
LOCUS
DEFINITION Homo sapiens mRNA for hRANKL 2, complete cds.
ACCESSION AB061227
VERSION AB061227.1 GI:16610212

KEYWORDS
SOURCE Homo sapiens cDNA to mRNA.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (sites)

Ikedo, T., Kuroyama, H. and Hirokawa, K.

TITLE

Human RANKL isoform

JOURNAL

2 (bases 1 to 911)

Ikedo, T. and Kuroyama, H.

REFERENCE

Submitted (02-MAY-2001)

Direct Submission

and Dental University, Pathology and Immunology; 1-5-45 Yushima,

Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.phn2@med.tmd.ac.jp,

Tel: 81-3-5803-5176, Fax: 81-3-5803-0123)

Location/Qualifiers

1. 911

/organism="Homo sapiens"

/db_xref="taxon:9606"

99. 911

/codon_start=1

/product="hRANKL 2"

/protein_id="BAB71768.1"

/db_xref="GI:16610212"

/translation="MEVALIGLGLQVVCVSALEFFYRAQMDPNRISDGHICVIRIL

RLHENAADPTLESQDRIIPDSGRIRKQAFQGVKELQHVQSQHIRAEKAVDG

SWLDAKRSKLEAOPFAHLLTNATIDPSGSHKVSLSVYHDKGNARKISNMTFSNKL

VNQGFFYLANKICFRHHHTSGDLATEYLQIMLVYVTKTSIKIPSSHTLMKGGSTKYS

GNSEPHYSINVGFFKLRSGEISIEVSNESLDDPDADATFFGAFKVRDID"

BASE COUNT 253 a 211 c 217 g 230 t

ORIGIN

Query Match 89.9%; Score 858; DB 9; Length 911;
Best Local Similarity 95.5%; Pred. No. 4.6e-168;
Matches 911; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 ATGCGCCGCCGACAGAGACTACACAGTACTGCGTGGCTCGGAGAGATGGCGGC 60
|||||
Db 1 ATGCGCCGCCGACAGAGACTACACAGTACTGCGTGGCTCGGAGAGATGGCGGC 60
QY 61 GGCCTCCGAGACCCCGACGACGAGGGGCCCTCCACGCCGCCGCCGCCGCCACCA 120
|||||
Db 61 GGCCTCCGAGACCCCGACGAGGGGCCCTCCACGCC----- 96
QY 121 CCCCCCGCCGCTCCGCTCATGTTCTGTCGCTCTGGGGCTGGGGGCTGGCGCAGTT 180
|||||
Db 97 -----CCATGTTCTGTCGCTCTCTGGGGCTGGGGGCTGGCGCAGTT 137
QY 181 GTCTGCGAGCGCGCCGCTCTCTCTATTTTACAGAGCGAGATGATCTTAATATATCA 240
|||||
Db 138 GTCTGCGAGCGCGCCGCTCTCTCTATTTTACAGAGCGAGATGATCTTAATATATCA 197
QY 241 GAAGATGGCACTCACTCATTTATAGAAATTTGAGACTCCATGAATAATGCAATTTTCAA 300
|||||
Db 198 GAAGATGGCACTCACTCATTTATAGAAATTTGAGACTCCATGAATAATGCAATTTTCAA 257
QY 301 GACCAACTCTGGAGACTCAAGATACAAATTAATATACCTGATTCATAGAGATTTAA 360
|||||
Db 258 GACCAACTCTGGAGACTCAAGATACAAATTAATATACCTGATTCATAGAGATTTAA 317
QY 361 CAGGCTTTTCAAGAGGCTGTGCAAAAGAAATTACACATATCGTTGGATCAGACATTC 420
|||||
Db 318 CAGGCTTTTCAAGAGGCTGTGCAAAAGAAATTACACATATCGTTGGATCAGACATTC 377
QY 421 AGACGAGAGAAAGCATGTGTGATGCTCATGTGTTAATCTGGCCAGAGAGACATCTT 480
|||||
Db 378 AGACGAGAGAAAGCATGTGTGATGCTCATGTGTTAATCTGGCCAGAGAGACATCTT 437
QY 481 GAAGCTGACCTTTTGGCTCATCTCATTTAATGSCACCCAGATCCCATCTGTTCCCAT 540
|||||
Db 438 GAAGCTGACCTTTTGGCTCATCTCATTTAATGSCACCCAGATCCCATCTGTTCCCAT 497
QY 541 AAGTGAAGTCTGCTCTCTGTGGTACCATGATCGGGGTTGGCCCAAGATCTCCAACTACT 600
|||||
Db 498 AAGTGAAGTCTGCTCTCTGTGGTACCATGATCGGGGTTGGCCCAAGATCTCCAACTACT 557
QY 601 TTATGCAATGGAACAACTAATAGTAAATCAGATGCGCTTTTATACCTGATGCCAATTT 660
|||||
Db 558 TTATGCAATGGAACAACTAATAGTAAATCAGATGCGCTTTTATACCTGATGCCAATTT 617
QY 661 TGCCTTGACATCATGAACCTTCAGAGACCTACGATGATCTTCAACTAATGATG 720
|||||
Db 618 TGCCTTGACATCATGAACCTTCAGAGACCTACGATGATCTTCAACTAATGATG 677
QY 721 TACGTCACATAAACACAGATCAAAATCCCAAGTCTCATACCTGATGAAGAAGAGAAC 780
|||||
Db 678 TACGTCACATAAACACAGATCAAAATCCCAAGTCTCATACCTGATGAAGAAGAGAAC 737
QY 781 ACCAAGTATGTCAGGAATTCGAAATTCATTTTATTCATGAACGATGATGATTT 840
|||||
Db 738 ACCAAGTATGTCAGGAATTCGAAATTCATTTTATTCATGAACGATGATGATTT 797
QY 841 TTAAAGTACGCTGTGAGAGAGAAATTCAGATCGAGTCTCCAAACCCCTCTACTGAT 900
|||||
Db 798 TTAAAGTACGCTGTGAGAGAGAAATTCAGATCGAGTCTCCAAACCCCTCTACTGAT 857
QY 901 CCGGATCGAGATGCAACATCTTTGGGCTTTTAAAGTTCGAGATATGATTGA 954
|||||
Db 858 CCGGATCGAGATGCAACATCTTTGGGCTTTTAAAGTTCGAGATATGATTGA 911

RESULT 8

AB064270 972 bp mRNA linear PRI 26-DEC-2001
LOCUS
DEFINITION Homo sapiens hRANKL 2-2 mRNA for receptor activator of nuclear
factor kappa B ligand 2-2, complete cds.
ACCESSION AB064270
VERSION AB064270.1 GI:18143620

KEYWORDS	Homo sapiens cDNA to mRNA.
SOURCE	Homo sapiens
ORGANISM	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Ikeda,T., Kuroyama,H. and Hirokawa,K. 1 (sites)
AUTHORS	Determination of human RANKL isoforms Unpublished
TITLE	2 (bases 1 to 972) Ikeda,T. and Kuroyama,H. Direct Submission
JOURNAL	Submitted (25-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School, Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan (E-mail:tooru.ph@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
FEATURES	Location/Qualifiers
source	1..972
gene	/organism="Homo sapiens" /db_xref="taxon:9606" 160..972
CDS	/gene="RANKL 2-2" 160..972 /gene="hRANKL 2-2" /codon_start=1 /product="receptor activator of nuclear factor kappa B ligand 2-2" /protein_id="BAB76695.1" /db_xref="GI:18143621" /translation="MEVALDGLGVCSVALEFFFRADMPNRISEDGTHCIYRLIL RLHNADFODTTLESODTKILPDCSRIRKQAFDOAVOKELIIGHOSHIRAKLVMDG SMDLARSKLEAPFAHLITINATIDPSGSHVSLSSWHDGRMAKSINTFSGKLIL VNQGFEYLIVANICFRHETEGDLATELYVMVTYSIKIPSPHTLMGGSTRKYNS GNSFHFPIVNGEFPRLRSEGEISVSNPSLLDPQDAITYEARFRVID"
BASE COUNT	270 a 219 c 249 g 234 t
ORIGIN	
Query Match	86.2%; Score 822.2; DB 9; Length 972;
Best Local Similarity	99.0%; Pred. No. 1.3e-160;
Matches 827; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
OY	120 GCCCCCCCGCCCTGCCCTCCATTTCGTGGCCCTCTGGGCGTGGGCCAGCT 179
DB	138 GCGGCGCCCGGAGCCCGCCTCCATGTTCTGGCCCTCTGGGCGTGGGCCAGCT 197
OY	180 TCTTGACAGCGTCGCCCTGTTCTTCTATTTCAGACCGCAGATGCATCTTAAGAATTC 239
DB	198 TGCTGCAAGCGTCCGCCCTGTTCTTCTATTTCAGACCGCAGATGCATCTTAAGAATTC 257
OY	240 AGAAGATGGCACTACTCATTTATAGATTTTGAGACTCCATGAANAATGCAGATTTCGA 299
DB	258 AGAAGATGGCACTACTCATTTATAGAAATTTTGAGACTCCATGAANAATGCAGATTTCGA 317
OY	300 AGACAACACTCTGGAGATCAAGATACAAAATTAATACCCTGATTCATGTAGAGAAATAA 359
DB	318 AGACAACACTCTGGAGATCAAGATACAAAATTAATACCCTGATTCATGTAGAGAAATAA 377
OY	360 ACAGGCTTTTCAAGAGCTGTGCAAAAGAAATTACAACATATCGTTGGATCACAGACAT 419
DB	378 ACAGGCTTTTCAAGAGCTGTGCAAAAGAAATTACAACATATCGTTGGATCACAGACAT 437
OY	420 CAGAGCAGAAAGAGATGGATGGTGCATGGTTGATGTGGCCAAAGAGACAAAGCT 479
DB	438 CAGAGCAGAAAGAGATGGATGGTGCATGGTTGATGTGGCCAAAGAGACAAAGCT 497
OY	480 TGAAGCTCAGCCTTTTGGTCATCTCACTATTAAATGCCACGCACATCCCATTTGGTCCA 539
DB	498 TGAAGCTCAGCCTTTTGGTCATCTCACTATTAAATGCCACGCACATCCCATTTGGTCCA 557
OY	540 TAAAGTAGCTGTCTCTTGGTACATGATCGGGGTTGGGCCAAAGATCTCAACATGAC 599

	Db	558	TAAAGGACTCTGTCTTGGACCATGATCGGGGTGGCCGAAGATCTCCAACATGAC	617
Oy	600	TTTTACCATTGGAACAATAATGTTATATAGAGTAGGCCTTTTATTACCTGTATGCCAACAT		659
Db	618	TTTTACCAATGGAAAACTAATGTTAATGAGATGGCTTTTATTACCTGTATGCCAACAT		677
Oy	660	TTTGCTTCGACATCATTGAACATTCAGAGGAGACCTACAGATATCTTCACACTAATGTT		719
Db	678	TTGCTTTGCATCATGTAACCTTCAGNACCTAGCTACAGATATCTTCACACTAATGTT		737
Oy	720	GTAACGCTACTAAAACACGATCAAAATCCCAGATTCCTCATACCTGATGAAGAAGGAAG		779
Db	738	GTAACGCTACTAAAACACGATCAAAATCCCAGATTCCTCATACCTGATGAAGAAGGAAG		797
Oy	780	CACCAAGTTTGTGTGAGGGAATTCGAATTCATTTTTCCTCATTAACGTTGGTGATT		839
Db	798	CACCAAGTTTGTGTGAGGGAATTCGAATTCATTTTTCCTCATTAACGTTGGTGATT		857
Oy	840	TTTTAAGTTACGCTCGAGAGGAATCGATCGATCGATCGATCGATCGATCGATCGATCGA		899
Db	858	TTTTAAGTTACGCTCGAGAGGAATCGATCGATCGATCGATCGATCGATCGATCGATCGA		917
Oy	900	TCCGATGATGAGTGAACATCTTTGGGCTTTTAAAGTTGAGATPATNGATTGA		954
Db	918	TCCGATGATGAGTGAACATCTTTGGGCTTTTAAAGTTGAGATPATNGATTGA		972
RESULT	9			
LOCUS	AB064268	818 bp	mRNA	linear PRI 26-DEC-2001
DEFINITION	Homo sapiens hRANKL 3 mRNA for receptor activator of nuclear factor kappa B ligand 3, complete cds.			
ACCESSION	AB064268			
VERSION	AB064268.1	GI:18143616		
KEYWORDS	.			
SOURCE	Homo sapiens cDNA to mRNA.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (sites)			
AUTHORS	Ikeda,T., Kuroyama,H. and Hirokawa,K			
JOURNAL	Determination of human RANKL isoforms			
TITLE	Unpublished			
REFERENCE	2 (bases 1 to 818)			
AUTHORS	Ikeda,T. and Kuroyama,H.			
JOURNAL	Direct Submission			
TITLE	Submitted (23-JUN-2001) Tohru Ikeda, Tokyo Medical and Dental University, Department of Pathology and Immunology, Graduate School; Yushima 1-5-45, Bunkyo, Tokyo 113-8519, Japan			
	(E-mail: toru.phn2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)			
FEATURES	Location/Qualifiers			
source	1..818			
	/organism="Homo sapiens"			
gene	/db_xref="taxon:9606"			
	84..818			
	/gene="hRANKL 3"			
CDS	84..818			
	/gene="hRANKL 3"			
	/codon_start=1			
	/product="receptor activator of nuclear factor kappa B ligand 3"			
	/protein_id="BAB79693.1"			
	/db_xref="GI:18143617"			
	/translation="MDPNRSIEDQTHICIVRLIRHENADFDOTTLSESODTKLIIPDSCRRIQAQFGAVQKELONIGVSOHIIRAFAWVGSMILDAKSKLEADPFALHTTNADI PSSGHSLSSWHDRGMARIMNTFENGLIYNOSGFYLVANICFRHNETHSGDLAT EYLQAWYVTIKTSIKIPSSHTLKMGSGSTKWMSGNSEHFYSINVGCFKLRSDEPISIEVNSPSLLDDDOATITGAKRVKDID"			
BASE COUNT	243 a	173 c	184 g	218 t
ORIGIN				

Query Match 82.8%; Score 790; DB 9; Length 818;
 Best Local Similarity 98.8%; Pred. No. 5.9e-154;
 Matches 796; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

149 TGGCGCTCTCTGGGCTGGGCGGAGGTTCTGACAGGTCGCCCTGTTCTTCTATT 208
    ||||| 1 |||||
Db 13 TGGCGCGACACAAAGAGGGGTGGCCAGGTGTCTGACAGGTCGCCCTGTTCTTCTATT 72
    |||||

QY 209 TCAGAGCGCAGATGATCTTAATATATCAAGATGCGACTCTGCTATTATGAA 268
    |||||
Db 73 TCAGAGCGCAGATGATCTTAATATATCAAGATGCGACTCTGCTATTATGAA 132
    |||||

QY 269 TTTTGAGAGCTCCATGAAATGCAAGTTTTCAGACACAACCTGAGAGTCAAGATGCAA 328
    |||||
Db 133 TTTTGAGAGCTCCATGAAATGCAAGTTTTCAGACACAACCTGAGAGTCAAGATGCAA 192
    |||||

QY 329 AATTAAATACGTATGATGTAGAGAAATTAACAGGCTTTCAAGAGAGCTGTGCAAAAG 388
    |||||
Db 193 AATTAAATACGTATGATGTAGAGAAATTAACAGGCTTTCAAGAGAGCTGTGCAAAAG 252
    |||||

QY 389 AATTAAACATATGCTGGTGCATCAGACATCAGACAGAGAAAGCATGGTGCATGGCT 448
    |||||
Db 253 AATTAAACATATGCTGGTGCATCAGACATCAGACAGAGAAAGCATGGTGCATGGCT 312
    |||||

QY 449 CATGGTTAGATCTGGCCCAAGAGAGAGCATTTGAAGCTCAGGCTTTTCTCATCTCACTA 508
    |||||
Db 313 CATGGTTAGATCTGGCCCAAGAGAGAGCATTTGAAGCTCAGGCTTTTCTCATCTCACTA 372
    |||||

QY 509 TTAATGCCACCGACATCCCATCTGGTCCCATTAAGTAGTCTGTCTCTTGTTGATGACATG 568
    |||||
Db 373 TTAATGCCACCGACATCCCATCTGGTCCCATTAAGTAGTCTGTCTCTTGTTGATGACATG 432
    |||||

QY 569 ATCGGGGTTGGGGCCCAAGATCTCCAAACATGACTTTTGAAGAGAACTAATAGTTAATC 628
    |||||
Db 433 ATCGGGGTTGGGGCCCAAGATCTCCAAACATGACTTTTGAAGAGAACTAATAGTTAATC 492
    |||||

QY 629 AGGATGGCTTTTATCTACCTGATGCGCAACATTTGCTTTCAGACATGAAACTTCAGAG 688
    |||||
Db 493 AGGATGGCTTTTATCTACCTGATGCGCAACATTTGCTTTCAGACATGAAACTTCAGAG 552
    |||||

QY 689 ACCTAGCTACAGAGATGATCTTCAACTAATGCTGTACGTCATTAACACAGCATCAAAATCC 748
    |||||
Db 553 ACCTAGCTACAGAGATGATCTTCAACTAATGCTGTACGTCATTAACACAGCATCAAAATCC 612
    |||||

QY 749 CAAGTTTCATACCTCGTGAAGAGAGAGACACCAAGATGTGTCAGAGAAATCTGAT 808
    |||||
Db 613 CAAGTTTCATACCTCGTGAAGAGAGAGACACCAAGATGTGTCAGAGAAATCTGAT 672
    |||||

QY 809 TCCATTTTATTCATTAACGTTGGTGGATTTTAAAGTTACGCTCTGAGAGAAATCA 868
    |||||
Db 673 TCCATTTTATTCATTAACGTTGGTGGATTTTAAAGTTACGCTCTGAGAGAAATCA 732
    |||||

QY 869 GCATGAGAGTCTCAACCCCTCTTACGTGATCGGATCGAGATCAACATATCTTTGGGG 928
    |||||
Db 733 GCATGAGAGTCTCAACCCCTCTTACGTGATCGGATCGAGATCAACATATCTTTGGGG 792
    |||||

QY 929 CTTTAAAGCTTGAGATATAGATGA 954
    |||||
Db 793 CTTTAAAGCTTGAGATATAGATGA 818
    |||||

```

RESULT 10

AB037599 930 bp mRNA linear PRI 06-APR-2000
 LOCUS AB037599 Homo sapiens mRNA for SODF/TRANCE, complete cds.
 DEFINITION AB037599 1 GI:6863047
 ACCESSION
 VERSION SODF/TRANCE; SODF/TRANCE.
 KEYWORDS Homo sapiens male tongue epithelial-like squamous cell carcinoma
 SOURCE cell_line:SCC-4 CDNA to mRNA.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (sites)
 AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.
 TITLE Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation

JOURNAL Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)

MEDLINE 20175237

REFERENCE 2 (bases 1 to 930)

AUTHORS Nagai,M., Kyakumoto,S. and Sato,N.

JOURNAL

Direct Submission
 Submitted (26-JAN-2000) Masazumi Nagai, Iwate Medical University
 School of Dentistry, Department of Biochemistry, 19-1 Uchiyama,
 Morioka, Iwate 020-8505, Japan (E-mail:mnagai@iwate-med.ac.jp,
 Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)

FEATURES

source

1. 930

/organism="Homo sapiens"

/db_xref="taxon:9606"

/sex="male"

/cell_line="SCC-4"

/cell_type="epithelial-like squamous cell carcinoma"

/tissue_type="tongue"

/gene="sodf/Trance"

/gene="sodf/Trance"

/gene="sodf/Trance"

/product="SODF/TRANCE"

/codon_start=1

/protein_id="BA9048.1"

/translation="MDPNRISDEGTHCYRIERLEHNAEDFDLTLESQTKLPDSCR
 RIKOAFDGAOKELQHVQSHIRAKRAMVDSWDLARKSKLEAPFAHLITNAYDI
 PEGSHKYSLSWYHDSRMKISMTFSNGKLIYNOGFYLYLVANICFRHHEISGLAT
 EYLOIMVYVTKTSIKIPISSHHTLKGSGTSKIVWSNFEHFSINVGFFKLRSGEELSI
 EVNSPLDDDDQATYFAGFKVDDID"

BASE COUNT 283 a 184 c 200 g 260 t 3 others

ORIGIN

Query Match 77.5%; Score 739; DB 9; Length 930;

Best Local Similarity 100.0%; Pred. No. 2.3e-143;
 Matches 739; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 216 GCAGATGATCCTATATATATATATATATATATATATATATATATATATATATAT 275
    |||||
Db 91 GCAGATGATCCTATATATATATATATATATATATATATATATATATATATATAT 150
    |||||

QY 276 ACTCCATGAAATGCAATTTTCAAGACACAACCTGTGAGAGCTCAAGATACAAATTAAT 335
    |||||
Db 151 ACTCCATGAAATGCAATTTTCAAGACACAACCTGTGAGAGCTCAAGATACAAATTAAT 210
    |||||

QY 336 ACCCTATTCATGTAGAGAAATTAACAGGCTTTCAAGAGAGCTGTGCAAAAGAAATTA 395
    |||||
Db 211 ACCCTATTCATGTAGAGAAATTAACAGGCTTTCAAGAGAGCTGTGCAAAAGAAATTA 270
    |||||

QY 396 ACATATGCTTGATACACAGACATATGAGAGAGAAAGCATGTGATGCTCATAGGTT 455
    |||||
Db 271 ACATATGCTTGATACACAGACATATGAGAGAGAAAGCATGTGATGCTCATAGGTT 330
    |||||

QY 456 AGATCTGGCCAAAGAGAGACCAAGCTTGAAGCTTTCATCTCATCTCATATTAATGC 515
    |||||
Db 331 AGATCTGGCCAAAGAGAGACCAAGCTTGAAGCTTTCATCTCATCTCATATTAATGC 390
    |||||

QY 516 CACGAGATCCCATCTGTTCCATATATATATATATATATATATATATATATATATAT 575
    |||||
Db 391 CACGAGATCCCATCTGTTCCATATATATATATATATATATATATATATATATATAT 450
    |||||

QY 576 TTGGGCCAAGATCTCAACATGACTTTTGAAGAGAGAAACTAATATATATATATATAT 635
    |||||
Db 451 TTGGGCCAAGATCTCAACATGACTTTTGAAGAGAGAAACTAATATATATATATATAT 510
    |||||

QY 636 CTTTAAATACCTGTATGCCAATGCTTTCATATGATATGAAACTTAGAGAGACTGAC 695
    |||||

```

Db 511 CTTTATTTACCTGTATGCCAACATTTGCTTTCGACATCATGAATCTCAGAGACCTAGG 570
Qy 696 TACAGATATCTTCACTAATAGTGTACGCTACTAAACAGCATGAATCCCAAGTTC 755
Db 571 TACAGATATCTTCACTAATAGTGTACGCTACTAAACAGCATGAATCCCAAGTTC 630
Qy 756 TCAATACCTGTATGAAGAGAGAGACACCAATTTGGTCAGGAAATTCGAATTCATTT 815
Db 631 TCATACCTGTATGAAGAGAGAGACACCAATTTGGTCAGGAAATTCGAATTCATTT 690
Qy 816 TTTATTCATTAACGCTGTGGGATTTTAAAGTTACGCTGTGAGAGAAATCAGCATGCA 875
Db 691 TTTATTCATTAACGCTGTGGGATTTTAAAGTTACGCTGTGAGAGAAATCAGCATGCA 750
Qy 876 GGTCTCCAAACCCCTCTTACTGATCCGGATCAGATGCAATCTTTGGGCTTTTAA 935
Db 751 GGTCTCCAAACCCCTCTTACTGATCCGGATCAGATGCAATCTTTGGGCTTTTAA 810
Qy 936 AGTTGAGATATAGATTGA 954
Db 811 AGTTGAGATATAGATTGA 829

RESULT 11
AX201362
LOCUS AX201362 2390 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 41 from Patent WO0153486.
ACCESSION AX201362
VERSION AX201362.1 GI:15391175

KEYWORDS
SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gunney, A.L.,
Hillan, K.J., Marsters, S.A., Pan, J., Pictel, R.M., Roy, M.A., Smith, V.,
Stone, D.M., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 41 26-JUL-2001;

TITLE
JOURNAL
Genentech, Inc. (US)

FEATURES
source 1..2390
Location/Qualifiers

BASE COUNT 778 a 417 c 506 g 688 t 1 others

ORIGIN

Query Match 77.5%; Score 739; DB 6; Length 2390;
Best Local Similarity 100.0%; Pred. No. 2.5e-143;
Matches 739; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 GCAGATGATCTTAATAGATATCAGAAAGATGCACATCTTATATAGATTTTGGAG 275
Db 521 GCAGATGATCTTAATAGATATCAGAAAGATGCACATCTTATATAGATTTTGGAG 580
Qy 276 ACTGCATGAATAATGACATTTTCAAGACACAACTCTGAGAGTCAAGATCAAAATTAAT 335
Db 581 ACTGCATGAATAATGACATTTTCAAGACACAACTCTGAGAGTCAAGATCAAAATTAAT 640
Qy 336 ACTGCATGATCTGATGAGAAATTAAGAGGCTTCAAGAGGCTTGAAGAAAGAAATTAACA 395
Db 641 ACTGCATGATCTGATGAGAAATTAAGAGGCTTCAAGAGGCTTGAAGAAAGAAATTAACA 700
Qy 396 ACATATCTTGATCAGACATCAGACAGAGAGAAAGCGATGGTGGATGGCTCATGCTT 455
Db 701 ACATATCTTGATCAGACATCAGACAGAGAGAAAGCGATGGTGGATGGCTCATGCTT 760
Qy 456 AGATCTGGCCAAAGAGGAGCAAGCTTGAAGCTCAGACCTTTGGCTCATCTCATTAATGC 515
Db 761 AGATCTGGCCAAAGAGGAGCAAGCTTGAAGCTCAGACCTTTGGCTCATCTCATTAATGC 820

Qy 516 CACCGACATCCCATCTGTGTTCCCATTAAGTAGTCTGCTCTTGGTACCATGATCGGG 575
Db 821 CACCGACATCCCATCTGTGTTCCCATTAAGTAGTCTGCTCTTGGTACCATGATCGGG 880
Qy 576 TTGGCCAAAGATCTCCACATGATGACTTTAGCAATGGAAACTAATAGTATCAGATGG 635
Db 881 TTGGCCAAAGATCTCCACATGATGACTTTAGCAATGGAAACTAATAGTATCAGATGG 940
Qy 636 CTTTATTTACCTGTATGCGCAATTTGCTTTCGACATCATGAAACTTCAGAGACCTAGC 695
Db 941 CTTTATTTACCTGTATGCGCAATTTGCTTTCGACATCATGAAACTTCAGAGACCTAGC 1000
Qy 696 TACAGAGATCTTCAACTAATAGTGTACGCTACTTAAACGACATCAAAATCCCAAGTTC 755
Db 1001 TACAGAGATCTTCAACTAATAGTGTACGCTACTTAAACGACATCAAAATCCCAAGTTC 1060
Qy 756 TCATACCTGTATGAAGAGAGAGACACCAAGTATTTGGTCAGGAAATTCGAATTCATTT 815
Db 1061 TCATACCTGTATGAAGAGAGAGACACCAAGTATTTGGTCAGGAAATTCGAATTCATTT 1120
Qy 816 TTTATTCATTAACGCTGTGGGATTTTAAAGTTACGCTGTGAGAGAGAAATCAGCATGCA 875
Db 1121 TTTATTCATTAACGCTGTGGGATTTTAAAGTTACGCTGTGAGAGAGAAATCAGCATGCA 1180
Qy 876 GGTCTCCAAACCCCTCTTACTGATCCGGATCAGATGCAACATCTTTGGGCTTTTAA 935
Db 1181 GGTCTCCAAACCCCTCTTACTGATCCGGATCAGATGCAACATCTTTGGGCTTTTAA 1240
Qy 936 AGTTGAGATATAGATTGA 954
Db 1241 AGTTGAGATATAGATTGA 1259

RESULT 12
AF013171

LOCUS AF013171 1823 bp mRNA linear PRI 19-SEP-1997

DEFINITION Homo sapiens TNF-related ligand TRANCE mRNA, partial cds.
ACCESSION AF013171
VERSION AF013171.1 GI:2411499

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M.,
Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
and Choi, Y.

TITLE
JOURNAL
TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)

REFERENCE

2 (bases 1 to 1823)

Wong, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y.
Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA

TITLE
JOURNAL
Rockefeller University, 1230 York Ave., New York, NY 10021, USA

FEATURES
source 1..1823
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="13q14"
/cell_type="thymocyte"
/note="encodes extracellular domain"
/note="TNF-related ligand"
/note="TNF-related ligand"
/codon_start=1
/product="TRANCE"
/protein_id="AAC51762.1"
/db_xref="GI:2411500"
/translation="OMDPNRISDEGTHCIYRILRLHENADEFDTTLESODTKLIPDSC

misc_feature

CDS

BASE COUNT 569 a 305 c 380 g 569 t
 ORIGIN
 RRIKQAFQAVOKELQHVIGSÖHTRAEKAMVDGSLDLAKRSKLEQPRHILNATD
 IPSGSHKVSLSWYHDGWMCKISNMTEFSNKLIVNDGEFYLLANICFRHETSGDIA
 TEXTOLMAYVTKTSIKIPSSHTLMKGGSTKYWSGNSEHFHYSINVGGFELRSGEELS
 IEVSNPDLPPDDATYFGAFKVRDID"

Query Match 76.9%; Score 733.2; DB 9; Length 1823;

Best Local Similarity 99.6%; Pred. No. 3.9e-142;

Matches 735; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 217 CAGATGATCCTAATAGAAATCAGAGATGGGACTCTCTGCTATTATAGATTTTGA 276
 DB 1 CAGATGATCCTAATAGAAATCAGAGATGGGACTCTCTGCTATTATAGATTTTGA 60
 QY 277 CTTCCATGAAATGAGATTTTCAAGACACACTCTGGAGAGTCAAGATACAAATTAATA 336
 DB 61 CTTCCATGAAATGAGATTTTCAAGACACACTCTGGAGAGTCAAGATACAAATTAATA 120
 QY 337 CTTGATTCATGTAGAGAAATTAACAGGCTTTCAAGAGCTGTGCAAAAGCATTAACA 396
 DB 121 CTTGATTCATGTAGAGAAATTAACAGGCTTTCAAGAGCTGTGCAAAAGCATTAACA 180
 QY 397 CATATCGTTGGATCAGACACATCAGACAGAGAGAGAGATGGTGGCTCATGGTTA 456
 DB 181 CATATCGTTGGATCAGACACATCAGACAGAGAGAGAGATGGTGGCTCATGGTTA 240
 QY 457 GATTCGGCCAAAG 516
 DB 241 GATTCGGCCAAAG 300
 QY 517 ACCGACATCCCATCTGGTCCCAATAAGTGAAGTCTCTCTGGTACATGATGGGGT 576
 DB 301 ACCGACATCCCATCTGGTCCCAATAAGTGAAGTCTCTCTGGTACATGATGGGGT 360
 QY 577 TGGGCCAATCTCCCAACATGACTTTTACATGAGAAATCAATAGTTATCAGATGGC 636
 DB 361 TGGGCCAATCTCCCAACATGACTTTTACATGAGAAATCAATAGTTATCAGATGGC 420
 QY 637 TTTTATACCTGTATGCCAACAATTTGCTTTCGACATCATGAAATCTCAGAGAGCTAGCT 696
 DB 421 TTTTATACCTGTATGCCAACAATTTGCTTTCGACATCATGAAATCTCAGAGAGCTAGCT 480
 QY 697 ACAGATATCTTCACTAATAGTGTACGTACCTAATAACAGAGATCAAAATCCCAAGTTCT 756
 DB 481 ACAGATATCTTCACTAATAGTGTACGTACCTAATAACAGAGATCAAAATCCCAAGTTCT 540
 QY 757 CATACCTGTATGAAG 816
 DB 541 CATACCTGTATGAAG 600
 QY 817 TATTCATTAACGTTGGTGGATTTTGAATTCAGTTCGCTGGAGAGAGAAATCCACATCGAG 876
 DB 601 TATTCATTAACGTTGGTGGATTTTGAATTCAGTTCGCTGGAGAGAGAAATCCACATCGAG 660
 QY 877 GTCCTCAACCCCTCTTACTAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGAT 936
 DB 661 GTCCTCAACCCCTCTTACTAGATCCGATCCGATCCGATCCGATCCGATCCGATCCGAT 720
 QY 937 GTTCGAGATATAGATTGA 954
 DB 721 GTTCGAGATATAGATTGA 738

RESULT 13
 AF187319 957 bp mRNA linear ROD 17-NOV-2000
 LOCUS AF187319
 DEFINITION Rattus norvegicus receptor activator of NF-kB ligand mRNA, complete cds
 ACCESSION AF187319
 VERSION AF187319.1 GI:10441420
 KEYWORDS

SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE 1 (bases 1 to 957)
 AUTHORS Xu, J., Tan, J.W., Huang, L., Gao, X.H., Laird, R., Liu, D., Wysocki, S. and Zheng, M.H.
 TITLE Cloning, sequencing, and functional characterization of the rat homologue of receptor activator of NF-kappaB ligand
 JOURNAL J. Bone Miner. Res. 15 (11), 2178-2186 (2000)
 MEDLINE 20540945
 REFERENCE 2 (bases 1 to 957)
 AUTHORS Xu, J.K. and Zheng, M.H.
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-1999) Orthopaedic Surgery, The University of Western Australia, Monash Ave., Nedlands, WA 6009, Australia
 FEATURES
 source
 CDS
 1..957
 /db_xref="taxon:10116"
 /note="ORF, osteoclast differentiation factor"
 /codon_start=1
 /product="receptor activator of NF-kB ligand"
 /protein_id="AA017031.1"
 /db_xref="GI:10441421"
 /translation="MRRANDYKYLRLSEEMSCDVPHEGFLHAPASAPAPPAASRPMLALIGLIGGVCSIALFLYERADMDNRLISEDSRCFYILRLRENTGLQDSTLESETEALPDSRCRMKAPGAGVADRELQHVQPRFSGVAPMAGSGMLDVARGLKPEQPFALHTINADIPSGSHKVSLSWYHDGWMCKISNMTEFSNKLIVNDGEFYLLANICFRHETSGVADYLDLMYVVKTSIKIPSSHTLMKGGSTKYWSGNSEHFHYSINVGGEFLRAGEEISYOVSNPDLPPDDATYFGAFKVRDID"

BASE COUNT 230 a 260 c 256 g 211 t
 ORIGIN

Query Match 70.8%; Score 675.4; DB 10; Length 957;
 Best Local Similarity 82.3%; Pred. No. 3.6e-130;
 Matches 788; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

QY 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGGCTGGAGAGATGGCGGC 60
 DB 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGGCTGGAGAGATGGCGGC 60
 QY 61 GGCCTGGAGAGCCGCGCAGAGAGGCGCCCTGCA--CGCCCGCGCGCTGCGCCGAC 117
 DB 61 GGCCTGGAGAGCCGCGCAGAGAGGCGCCCTGCA--CGCCCGCGCGCTGCGCCGAC 120
 QY 118 CAGCCCGCCGCGCGCTCCGCTCCATGTTGCTGGGCGCTCTGGGCGTGGGCGCCAG 177
 DB 121 CCGCCCGCCGCGCGCTCCGCTCCATGTTGCTGGGCGCTCTGGGCGTGGGCGCCAG 180
 QY 178 GTTGTCTGAGCGTGGCCCTGTTCTTATTTTCAAGAGCGCAGATGATCTTAATGAATA 237
 DB 181 GTTGTCTGAGCGTGGCCCTGTTCTTATTTTCAAGAGCGCAGATGATCTTAATGAATA 240
 QY 238 TCAGAGATGAGCACTACCTGCAATTTATAGATTTTGAAGTCTCCAGAAATGCAATTT 297
 DB 241 TCAGAGATGAGCACTACCTGCAATTTATAGATTTTGAAGTCTCCAGAAATGCAATTT 300
 QY 298 CAAAGACAACTGTGAGAGTCAAGATCAAAATTAATCTGATTCATGTAGAGAAAT 357
 DB 301 CAAAGACAACTGTGAGAGTCAAGATCAAAATTAATCTGATTCATGTAGAGAAAT 360
 QY 358 AAACAGCCTTTCAGAGAGCTGTGCAAAAGAAATTAACAATATGCTGGATCAGACAG 417
 DB 361 AAACAGCCTTTCAGAGAGCTGTGCAAAAGAAATTAACAATATGCTGGATCAGACAG 420
 QY 418 ATCAGAGCAGAGAAAGCAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 477
 DB 421 TTCTCAGAGAGTTCACGCTATGATGAGAGGTTGCTGCTGATGAGTGGCCCGCGGGGCAAG 480

Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
70.0%;	82.7%;	791;	0;	667.8;	10;	2225;
	Pred. No. 1.5e-128;		Mismatches 157;		Indels 9;	Gaps 2;
1	ATGGCGCGCGCCAGCAGAGACTACACCAAGTACTGCTGCGCTCGGAGAGATGGGCGGC	60				
137	ATGGCGCGCGCGCCAGCAGAGACTACACCAAGTACTGCGCGCGAGAGATGGGCGGC	196				
61	GGCCCGCGAGCGCCGCGCAGAGAGGCGCCCTGTGACGCGCCGCGC---GGCCGCTGTGCGCGCGAC	117				
197	GGCCCGCGCGCGCGCGCAGAGAGGCGCGCCCTGTGACGCGCCGCGCCTTCTGACACGGGCTCGGCGC	256				
118	CAGCGCGCGCGCGCGCTCCGCTCCATGTTGCTGGGCGCTCTGGGGCTGGGGCTGGGGCGAG	177				
257	CGCGCAGCGCGCGCGCGCTCCGCTCCATGTTGCTGGGCGCTCTGGGGCTGGGACTGGGGCGAG	316				
178	GTTGCTGCGAGCGTGGCGCGCTGTTCTTCAATTTTCAGAGGCGCAGATGAGATGCATAATGAGTA	237				
317	GTGGCTGCGACAGATCGCTCTGTTCTGTGACTTTTGAGCGCGCAGATGAGATGCATAATGAGTA	376				
238	TCAGAGAGTGGCACTGCATGATTTATATGAAATTTTGGAGACTGCATGAGAAATGCAAGATTTT	297				

QY	898	GATCCGATCAGATGCAACATACTTTGGGGCTTTTAAAGTTCGAGATATAGATTGA	954
Db	1031	GATCCGATCAAGATCGGACGCTACTTTGGGGCTTTCAAGTTCAGGACATAGACTTGA	108

RESULT	15		
E34350			
LOCUS	E34350	951 bp	DNA
DEFINITION	DNA and process for producing protein by using the same.		
ACCESSION	E34350		
VERSION	E34350.1	GI:18624335	
KEYWORDS	JP 2000102390-A/5.		
SOURCE	Mus sp.		
			PAT 31-JAN-2002

BASE COUNT	231 a	267 c	248 g	205 t
ORIGIN				

Query Match	69.8%;	Score 666.2;	DB 6;	Length 951;
Best Local Similarity	82.5%;	Pred. No. 2.9e-128;		
Matches 790; Conservative	0;	Mismatches 158;	Indels 9;	Gaps 2;

[illegible]

```

0y      61 GGGCCCGGAGCCCCGCGACGAGGGCCCCCTTCGACGGCCCCGAC 11
          |||||  ||| |||||  |||||  |||  |  |||  |||
Db      61 GGGCCCGGCGTCCACACGAGGGGTCGCTGCACCCCGGCGCTTCGACCGGGCTCCGGCG 12

```

Qy 118 CAGCCCCCGCCGCTCCGGCTCATGTTCGTGGCCCTCCTGGGGCTGGGGCTGGGCCAG 17
+
Db 121 CCGCCACCGCGGCCTCCCGCTCATGTTCCTGGCCCTCCCTGGGGCTGGAGACTGGGCCAG 18

```

Oy 178 GTTGTCTGCAGCGCTGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGATA 23
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GTGGTCTGCAGCATCCGCTCTGTTCCTGTACTTTCAGAGCGCAGATGGATCCTAACAGATA 24

```

```
Oy      238 TCAGAAGATGGCACTCACTGCATTTTTAGACAATTTTGACGTAAAAATGCAGATTTTT    29  
        |||||   |||||||   |||||||   |||||||   |||||||   |||||||  
  
Db      241 TCAGAAGACAGCACTCACTGCTTTTATAGATCCGTGAGACTCATGAATAACGCCAGTTTTG    30
```

```

Oy 298 CAAGACACAACTCTGGAGAGTCAAGATCAAAATTATATACCTGATTCATGTAGGAGAAAT 35
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CAGGACTCGACTCTGGAGAGTGAACACAC-----ACTACCTGACTCCTGCAGAGAGGATG 35

```

[illegible]

| | | | |
|----|-----|---|------|
| OY | 418 | ATCAGAGCAGAAAACGATGGTGGATGCTCATGTTAGATCTGCGCCAGAGACGAC | 4177 |
| Db | 415 | TTCCTCAGAGAGCTCCACGCTATATGGAAGGCTCATGGTTGGATGGGCCACGCGAGG | 4174 |
| OY | 478 | CTTGAGAGTCAGCCCTTTTGGCTATCTCAGCTTTATATGCAACCGACATCCCATCTGGTTCC | 5375 |
| Db | 475 | CCTGAGGCCACGACCATTTGGCACACCTCACCATTCATATGCTGGCACATCCCATCGGGTTCC | 5343 |
| OY | 538 | CATAAAGTAGCTGTGCTCTTTGGTACCATGATGGGGTTGGGCCAAGATCTCCAATG | 5975 |
| Db | 535 | CATAAAGTCACTGTCTCTCTTGTTACACAGCATGAGAGCTGGGCCAAGATCTCTAATG | 5943 |
| OY | 598 | ACTTTTACCATGGAACCTATAGTTATGATGAGATGGCTTTTATACCTGTATGCCAC | 6575 |
| Db | 595 | ACGTTAAGCAACGGAACCTAAGGGTTTACCAAAATGGCTCTATTAACGTGTACGCCAC | 6543 |
| OY | 658 | ATTGCTTTGCACATCATGAACCTTCAGAGAGCCTAGCTACAGAGTATCTTCAACTATG | 7117 |
| Db | 655 | ATTGCTTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCACCTATG | 7143 |
| OY | 718 | GTGTACGTCACATAAACCCAGATCAAAATCCCAAGTCTCTACCCGTGATGAAGGAGA | 7777 |
| Db | 715 | GTGTATGTCTGTAAACACGATCAAAATCCCAAGTCTCTAATACGTGATGAAGGAGG | 7743 |
| OY | 778 | AGCACCAAGTATTGGTCAGGGAATTCGATTCATTTTATTCATTAACGTTGGTGA | 8337 |
| Db | 775 | AGCACGAAAAACCTGCTCGCGCAATTCGAAATTCACCTTTATTCATTAAGTTGGGGGA | 8343 |
| OY | 838 | TTTTTAAAGTTACGGTCGCGAGAGAATTCAGATCGAGTCTCCAAACCCCTCTTACTG | 8977 |
| Db | 835 | TTTTTCAAGCTCCGAGCTGGTGGAAGAAATTTAGCATTCAGTGTGTCCAAACCCCTCTGTG | 8943 |
| OY | 898 | GATCCGGATCAGAGATGACAATACTTTTGGGCTTTTAAAGTTCCAGATATATGATTGA | 9543 |
| Db | 895 | GATCCGGATCAAGATGCGACGACTTTTGGGCTTTTCAAGTTCCAGACATGAGACTGA | 9513 |

Search completed: July 8, 2002, 23:50:19
Job time: 13458 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 21:43:41 ; Search time 408.13 Seconds

(without alignments)
4013.271 Million cell updates/sec

Title: US-09-865-363-12

Sequence: 1 ATCGCGCCGCCACAGCA.....AAGTTCAGATATAGATTGA 954

Scoring table:

IDENTITY-NUC
Gapop 10.0 ; Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_032802:*

- 1: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 954 | 100.0 | 954 | 19 | AAV41378 |
| 2 | 954 | 100.0 | 954 | 19 | AAV41372 |
| 3 | 954 | 100.0 | 954 | 22 | AAO15311 |
| 4 | 954 | 100.0 | 954 | 22 | AAO08715 |
| 5 | 954 | 100.0 | 954 | 22 | AAO05904 |
| 6 | 954 | 100.0 | 2271 | 21 | AAZ99964 |
| 7 | 954 | 100.0 | 2274 | 19 | AAV70285 |
| 8 | 950.8 | 99.7 | 954 | 19 | AAV69887 |
| 9 | 739.4 | 77.5 | 741 | 19 | AAV69899 |

| | | | | | | |
|----|-------|------|------|----|----------|--------------------|
| 10 | 733.2 | 76.9 | 1823 | 20 | AAx80223 | Human TRANCE encod |
| 11 | 675.4 | 70.8 | 957 | 22 | AAx86481 | Rat osteoclast dif |
| 12 | 666.2 | 69.8 | 951 | 19 | AAx69900 | Nucleotide sequenc |
| 13 | 666.2 | 69.8 | 951 | 21 | AAx39156 | Mouse OBM nucleoti |
| 14 | 666.2 | 69.8 | 951 | 21 | AAx29965 | DNA encoding a mur |
| 15 | 666.2 | 69.8 | 951 | 21 | AAx49024 | Osteoclast format |
| 16 | 666.2 | 69.8 | 1538 | 19 | AAx69886 | Nucleic acid encod |
| 17 | 666.2 | 69.8 | 2191 | 19 | AAV41489 | Nucleotide sequenc |
| 18 | 666.2 | 69.8 | 2295 | 19 | AAV70284 | Human osteoprotege |
| 19 | 666.2 | 69.8 | 2299 | 21 | AAx29966 | DNA encoding a mur |
| 20 | 663 | 69.5 | 2237 | 20 | AAx80224 | Murine TRANCE enco |
| 21 | 615 | 64.5 | 1630 | 19 | AAV41377 | NF-KB receptor act |
| 22 | 615 | 64.5 | 1630 | 19 | AAV41371 | Murine receptor ac |
| 23 | 615 | 64.5 | 1630 | 22 | AAO15310 | Murine receptor ac |
| 24 | 615 | 64.5 | 1630 | 22 | AAO15310 | Murine receptor ac |
| 25 | 615 | 64.5 | 1630 | 22 | AAO08714 | Murine receptor ac |
| 26 | 526.6 | 55.1 | 1574 | 22 | AAH25526 | Murine RANKL (rece |
| 27 | 520.6 | 54.6 | 735 | 19 | AAV69898 | Nucleotide sequenc |
| 28 | 365.6 | 38.3 | 522 | 22 | AAx13369 | Nucleic acid encod |
| 29 | 325.4 | 34.1 | 2029 | 21 | AAx39155 | Mouse CDNA encodin |
| 30 | 276.4 | 29.0 | 564 | 21 | AAx29967 | DNA encoding osteo |
| 31 | 276 | 28.9 | 519 | 21 | AAx29968 | DNA encoding osteo |
| 32 | 247.2 | 25.9 | 519 | 21 | AAx29969 | DNA encoding osteo |
| 33 | 247.2 | 25.9 | 519 | 21 | AAx29972 | DNA encoding osteo |
| 34 | 231.2 | 24.2 | 519 | 21 | AAx29973 | DNA encoding osteo |
| 35 | 227.8 | 23.9 | 546 | 21 | AAx29971 | DNA encoding osteo |
| 36 | 209.8 | 22.0 | 564 | 21 | AAx29970 | DNA encoding osteo |
| 37 | 151.4 | 15.9 | 2026 | 21 | AAx39152 | Mouse OBM nucleoti |
| 38 | 119 | 12.5 | 254 | 20 | AAx56001 | Human tumor necro |
| 39 | 114.2 | 12.0 | 468 | 21 | AAx39153 | Human tumor necro |
| 40 | 70.4 | 7.4 | 1288 | 21 | AAx67833 | Fc-huNGP-1 (114-28 |
| 41 | 70.4 | 7.4 | 1345 | 21 | AAx67832 | Cell factor deriva |
| 42 | 69.4 | 7.3 | 656 | 21 | AAx38005 | GH-derived leader |
| 43 | 69.4 | 7.3 | 759 | 22 | AAI18398 | CMV-derived leader |
| 44 | 69.4 | 7.3 | 768 | 22 | AAI18399 | Ompa signal peptid |
| 45 | 69.4 | 7.3 | 801 | 22 | AAO03112 | |

ALIGNMENTS

| RESULT | 1 | ALIGNMENTS |
|----------|--|--|
| AAV41378 | standard; CDNA; 954 BP. | |
| ID | AAV41378 | |
| XX | AAV41378; | |
| AC | XX | |
| XX | XX | |
| DT | 08-OCT-1998 (first entry) | |
| DE | NF-KB receptor activator RANK ligand (RANKL) encoding CDNA. | |
| XX | XX | |
| XX | RANK; necrosis factor-kappa B; NF-KB; receptor activator; human; | |
| KW | Immune response; inflammatory response; toxic shock; sepsis; | |
| KW | RANKL; RANK ligand; tumor necrosis factor; TNF; ss. | |
| XX | XX | |
| OS | Homo sapiens. | |
| XX | XX | |
| FH | Key | Location/Qualifiers |
| FT | CDS | 1..954 |
| FT | | /*tag="a |
| XX | | /product="human RANKL (ligand for RANK)" |
| PN | W09828426-A2. | |
| XX | XX | |
| PD | 02-JUL-1998. | |
| XX | XX | |
| PF | 22-DEC-1997; | 97WO-US23775. |
| XX | XX | |
| PR | 14-OCT-1997; | 97US-0064671. |
| PR | 23-DEC-1996; | 96US-0059978. |
| PR | 07-MAR-1997; | 97US-0813509. |
| XX | XX | |
| PA | (IMMV) IMMUNEX CORP. | |

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI: 1998-377657/32.
DR P-PSDB; AAM69957.

XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells

XX Claim 25; Pages 59-60; 80pp; English.

XX This CDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappa (NF-kb)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kb, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kb by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening.

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

XX Query Match 100.0%; Score 954; DB 19; Length 954;

XX Best Local Similarity 100.0%; Pred. No. 5e-241;

XX Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCGCCAGACAGAGACTACACCAAGTACCTGCTGGCTGGAGAGATGGCGGC 60
DB 1 atgcgcgcgccagacagagactacaccaagctgctgctgagagagatggcggcg 60
QY 61 GGCCTGGAGACCCCGACAGAGGCGCCCTGCGAGCGCCGCGCGCTGGCGCGCACG 120
DB 61 ggcctggagaccccgacagagggccctgacgccccgcgcgctggcgcgcacg 120
QY 121 CCCCCGCGCGCTCCGCTCATGTTGTTGTCCTCTGCGGCTGGGCGTGGCCAGGTT 180
DB 121 cccccgcgcgctccgctcatgttggctctgctggtggcggtggcgagtt 180
QY 181 GTCTGACAGCTGCGCTGTTCTTCTATTTCAGAGCGGAGATGGATCTCTAATAGAAATCA 240
DB 181 gtctgacagctgcgctgttcttctatttcagagcgagatggatctctaatagaataca 240
QY 241 GAATATGGACATCTGATTAATAGAAATTTGACATCATGATGTAATGAGATTTTCAA 300
DB 241 gaatattggacatctgatttaataaatttgacatcatgattgtaattgagattttcaa 300
QY 301 GACACACTGTGAGAGTCAAGATACAAATTAATACCTGATTCATGAGAGATTTAAA 360
DB 301 gacacactgtgagagtgacagatacaaaatttaacctgattcatglaagagattaaa 360
QY 361 CAGGCTTTCAAGAGCTGTGCAAAAGAAATTACACATATGTTGGATCAGACATC 420
DB 361 caggctttcaagagctgtgcaaaagaaattacacatactgtgattccagacaatc 420
QY 421 AGAGCAGGAAGAGATGATGATGCTCATGTTAGATTGCGCAGAGAGAGCAAGCTT 480
DB 421 agagcaggaagagatgattgattgctcatgtttagatttgccgcaagagagagcaagctt 480
QY 481 GAAGCTCAGCTTTTGTCTATCTCATCTAATTAATGCGACGACATCCCTCTGTTCCAT 540

DB 481 gaagctcagcttttgcctatctcatctataatgcccacagcatccatctgttccat 540
QY 541 AAGTAGTCTGCTCTTGTGACATGATTCGGGGTGGGCAAGATCTCCAATGACT 600
DB 541 aagtagtctgctcttgtgacatgattcgagggtgggcaagatctccaatgact 600
QY 601 TTATGCAATGGAACCAATAGTAAATGAGATGCTTTTATTAATCTGTATGCCAATTT 660
DB 601 ttatgcaatggaaccaatagtaataatgagatgcttttatttaattacgtatgccaat 660
QY 661 TGCTTTGACATCATGAAACTTCAGAGACCTTACCTACAGATATCTTCAATGATG 720
DB 661 tgctttgacatcatgaaacttcagagaccttacctacagatattcttcaatgatg 720
QY 721 TACCTACTAAACCCACATCAAAATCCCAAGTTCTCATACCTGTATGAAAGAGAAC 780
DB 721 tacctactaaacccacatcaaaatcccaagttctcatacctgtatgaagagaaac 780
QY 781 ACCAAGTATTGTCAGGGAATTCGAATTCATTTTATTCATTAACGTTGGATTT 840
DB 781 accaagtattgtcagggaaatttcgaatttcatttatttcaataacglttgat 840
QY 841 TTTAAGTTACGCTGTGAGAGAGAAATCAGCATGAGGCTCCAAACCCCTTACTGAT 900
DB 841 ttttaagttacgctgtgagagagaaatcagcatgaggctccaaaccccttactgat 900
QY 901 CCGGATCAGATGCAACATACTTTGGGGCTTTTAAAGTTGAGATATATGATGA 954
DB 901 cgggatcagatgcaacatactttggggctttttaaagttgagatatatgata 954

RESULT 2

ID AAV41372 standard; cDNA; 954 BP.

AC AAV41372;

DT 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW Immune response; inflammatory response; toxic shock; sepsis;

KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

OS Homo sapiens.

FT Key location/Qualifiers

FT CDS 1..954 /tag= a

FT /product= "human RANKL (ligand for RANK)"

MO9828424-A2.

02-JUL-1998.

22-DEC-1997; 97WO-US23866.

14-OCT-1997; 97US-0064671.

23-DEC-1996; 96US-0059978.

07-MAR-1997; 97US-0813509.

(IMMV) IMMUNEX CORP.

Anderson DM, Galibert LJ, Maraskovsky E;

WPI: 1998-377655/32.
P-PSDB; AAM68293.

New isolated receptor activator of necrosis factor-kappa B - useful
for, e.g. developing products for regulating an immune or
inflammatory response, treating toxic shock or sepsis

are useful for regulating immune response and in screening for inhibitors of these receptors. The cytoplasmic domain of RANK is used in developing assays for inhibitors of signal transduction, e.g. for screening the molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful in ameliorating the negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, acute inflammatory reactions and the effects of bone resorption. RANK acts as an anti-apoptotic signal and rescue the cells that express RANK from apoptosis. Soluble forms of the receptor are used in vivo or in vitro based screening tests for agonists or antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B activation, or to inhibit transduction of a signal via RANK. RANK compositions are used in the development of both agonistic and antagonistic antibodies, or as an adjunct therapy for disease characterised by neoplastic cells that express RANK. Compounds that interfere with RANK/TRAF6 interactions are useful for modulating the formation of osteoclasts from osteoclast precursors and for modulating osteoclast function and activities. They are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is a cDNA encoding human RANK ligand (RANKL) protein.

Sequence 954 BP: 255 A; 239 G; 227 G; 233 T; 0 other;

Query Match 100.0%; Score 954; DB 22; Length 954;

Best Local Similarity 100.0%; Pred. No. 5e-241; Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCCGCGCCGAGACAGACATACCAAGTACCTGCTGGCTCGAGAGATGGCGCGC 60
 Db 1 atgcgccgcgcagagagagactaaccaagtaacctgctgctcgagagatggcgcgcg 60
 QY 61 GGGCCGGAGCCCGCAGAGAGGGCCCTGACAGCGCCCGCGCGCGCGCGAGACCGC 120
 Db 61 gggccggagcccgagagagggccctgacagcgcccgcgcgcgcgcgagacccag 120
 QY 121 CCCCCGCGCGCTCCGCCATGTTCTGCGCTCTGCGGCTGGGCTGGGCGCAGGTT 180
 Db 121 cccccgcgcgcctccgccatgttctgctgctctgctgctgctggcgctggcgaggtt 180
 QY 181 GTCTCAGCGTGGCCCTGTTCTTATTTCAGAGCGCAGAGGATCTTAATGAATATCA 240
 Db 181 gtctcagcggtggccctgttcttatttcagagcgagagatcttaataagaataca 240
 QY 241 GAAGATGGACATCATGATTTATAGAAATTTAGACATCCATGAAGAAGCAATTTTCA 300
 Db 241 gaagatggacatcatgatttatagaaattttagacatccatgaagaagcaattttcaa 300
 QY 301 GACACAACCTCTGAGAGATCAAGATACAAATTAATACCTGATTCAATGAGAAATTAA 360
 Db 301 gacacaacctctgagagatcaagatacaaatataatcctgattcaatgagaattaaa 360
 QY 361 CAGGCCCTTCAAGAGAGCTGTGCAAAAAGCAATTACAAATATGTTGGATCAAGACATAC 420
 Db 361 caggcccttcaagagagctgtgcaaaaagcaattacaaatattggtacaaagacaccc 420
 QY 421 AGAGCGAGAAAGCGATGGTGGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 421 agagcgagaaagcgatggatgatatgatatgatatgatatgatatgatatgatatgatat 480
 QY 481 GAGGCTCAGCCTTTGCTCATCTCACTAATTAATGCCAGCAGACATCCATCTGGTCCAT 540
 Db 481 gaggctcagcctttgctcatctcaactaataatgacacagacatccatctgltccat 540
 QY 541 AAAGTAGTCTGTCTTGTGATACCATGATCGGGTTGGGCGCAAGATCTCCAAACATGACT 600
 Db 541 aaagtgtgtctgtctgtgtacatgacatgacggtgtggcgcaagatctccaacatgact 600

QY 601 TTATGCAATGGAAGAACTAATAGTTAATCAGAGATGCTTTATACCTGATGCCAATTT 660
 Db 601 ttatgcaatggaagaaactaataatagtttaatacagagatgctttatacctgatacgcaactt 660
 QY 661 TGGTTTCAGATCATGAAAGCTTTCAGAGAGACCTTACATGATATCTTCAATTAATGCTG 720
 Db 661 tggtttcagatcatgaaagcttttcagagagaccttacctgatacttaactaaatgctg 720
 QY 721 TAGTCTCTTAAACCCAGCATCAAAATCCCAAGTTCATACCTGATGAAAGAGAGAGC 780
 Db 721 tagtctctttaaaccagcatcaaaatcccaagtctcatacctgataagagagagagc 780
 QY 781 ACCAAGATTTGTCAGAGAAATTCGAATTCATTTTATTCATTAACGTTGGTGATTT 840
 Db 781 accaagatttgtcagagaaattcgaatttcatttcatcttaacacgttggatgtt 840
 QY 841 TTTAAGTTACGCTGTGAGAGAAATTCAGATCGAGCTCCAAACCCCTCTTACTGAT 900
 Db 841 ttttaagttacgctgtgagagaaattcagatcgagctccaaacccctcttactgatt 900
 QY 901 CCGGATCAGATGCAACATCTTTGGGCTTTAAAGTTCGAGATATGATGA 954
 Db 901 ccggatcagatgcaacatctttgggctttaaagtctgagatatagatga 954

RESULT 4

AAD08715 standard; cDNA: 954 BP.

AAD08715;

04-SEP-2001 (first entry)

Human receptor activator of NF- χ B ligand (hRANKL) cDNA.

Human; receptor activator of NF- χ B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response;

chromosome 18q22.1; hRANKL; chromosome 13q14; transmembrane protein; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 1..954

FT /tag= a

product= "Human RANKL protein"

US6242213-B1.

05-JUN-2001.

22-DEC-1997; 97US-0995659.

23-DEC-1996; 96US-0059978.

07-MAR-1997; 97US-0077181.

14-OCT-1997; 97US-0064671.

(IMNV) IMMUNEX CORP.

Anderson DM;

WPI: 2001-407216/43.

P-PSDB; AAE04426.

New DNA molecules, useful for producing ligands (which are useful for

regulating immune response and in screening for inhibitors of NF- χ B

receptor activator) of the receptor activator of NF- χ B (RANK)

Claim 2; Column 61-64; 43pp; English.

The present invention relates to receptor activator of NF- χ B (RANK) cDNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane

XX Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other:

Query Match 100.0%; Score 954; DB 22; Length 954;
Best Local Similarity 100.0%; Pred. No. 5e-241;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCCGCGCCAGACAGACATACACCAAGTACCTGGCTGCTCGAGAGATGGCGGC 60
1 atggccgcgcagacagagactacacaaagctcgtgctcgagagatggcggc 60
61 GGGCCGGAGCCCGGACAGAGAGGCCCTCGACGCCCGCCGCTGGCGCCGACGAG 120
61 gggccggagcccgacagagagccctcgacgcccgccgctggcgccgacgag 120
61 gggccggagcccgacagagagccctcgacgcccgccgctggcgccgacgag 120
121 CCCCCCGCGCTCCCGTCATGTTCTGGCCCTCGTGGGGCTGGGGCTGGCGCAGGTT 180
121 cccccgcgcgcctccgctcatgttctggccctcgtggggctggggctggcgca 180
121 cccccgcgcgcctccgctcatgttctggccctcgtggggctggggctggcgca 180
181 GTCTGACAGCTCGCCCTGTTCTTCTATTTCAGAGCGCAGATGATCCTAATAGATATCA 240
181 gtctgacagctcgccctgttcttctatttcagagcgcatgatcctaataagatca 240
181 gtctgacagctcgccctgttcttctatttcagagcgcatgatcctaataagatca 240
241 GAAGATGACACTCATGATTTATGAAATTTGAGACTCCATGAAATGCAATTTTCAA 300
241 gaagatgacactcatgatttatgaaatttgagactccatgaaatgcaattttcaa 300
241 gaagatgacactcatgatttatgaaatttgagactccatgaaatgcaattttcaa 300
301 GACACAACTCTGAGAGATCAAGATCAAAATTAATACCTGATTCATGTAGAGAAATTA 360
301 gacacaaactctgagagatcaagatcaaaatataatctgattcatgtagagaaat 360
301 gacacaaactctgagagatcaagatcaaaatataatctgattcatgtagagaaat 360
361 CAGGCTTTCAGAGAGCTGTGCAAAAGAAATTAACAAATATGATGATGATGATGATGAT 420
361 caggcttttcagagagctgtgcaaaagaaatataacaaatattgtgagacagacac 420
361 caggcttttcagagagctgtgcaaaagaaatataacaaatattgtgagacagacac 420
421 AGAGCGAGAAAGCGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
421 agagcgagaaagcgatgtgatgatgatgatgatgatgatgatgatgatgatgatgat 480
421 agagcgagaaagcgatgtgatgatgatgatgatgatgatgatgatgatgatgatgat 480
481 GAAGCTCAGCCTTTTGTCTACTACTATTAATGATGATGATGATGATGATGATGATGAT 540
481 gaagctcagcctttgtctactactatataatgagacagacatccatctgttccat 540
481 gaagctcagcctttgtctactactatataatgagacagacatccatctgttccat 540
541 AAAGTATGCTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
541 aaagtatgctgctctctgctgctgctgctgctgctgctgctgctgctgctgctgct 600
541 aaagtatgctgctctctgctgctgctgctgctgctgctgctgctgctgctgctgct 600
601 TTATGCAATGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
601 ttaagcaatgaaatataatgctgctgctgctgctgctgctgctgctgctgctgctgct 660
601 ttaagcaatgaaatataatgctgctgctgctgctgctgctgctgctgctgctgctgct 660
661 TGCTTGCATCATGAAATTAAGAGAGCTGATGATGATGATGATGATGATGATGATGAT 720
661 tgcttgcacatgaaatataagagagctgctgctgctgctgctgctgctgctgctgct 720
661 tgcttgcacatgaaatataagagagctgctgctgctgctgctgctgctgctgctgct 720
721 TAGCTCACTAAACCAACCAATCAAAATGCTGATGATGATGATGATGATGATGATGAT 780
721 tagctcactaaaccaaaccatcaaaatcccaagctgctgctgctgctgctgctgctgct 780
721 tagctcactaaaccaaaccatcaaaatcccaagctgctgctgctgctgctgctgctgct 780
781 ACCAAGATTGCTCAGGGAATTCGAATTCATTTTATTCATTAAGCTGTGATGATTT 840
781 accaagattgctcagggaaatcgaattcgaattcgaattcgaattcgaattcgaattcga 840
781 accaagattgctcagggaaatcgaattcgaattcgaattcgaattcgaattcgaattcga 840
841 TTTAAGTTACGGTGTGAGAGAAATACAGATGAGATGATGATGATGATGATGATGATGAT 900
841 ttttaagttacgggttgagagaaatcacagatgagatgagatgagatgagatgagatgag 900
841 ttttaagttacgggttgagagaaatcacagatgagatgagatgagatgagatgagatgag 900
901 CCGGATACAGATGACATACATCTTTGGGGCTTTTAAAGTTGAGATATGATATGA 954
901 cgggatcacgattgacatactcttggggcttttaaaagttgagatatagattga 954
901 cgggatcacgattgacatactcttggggcttttaaaagttgagatatagattga 954

RESULT 6

AAZ99964
ID AAZ99964 standard; DNA; 2271 BP.

AAZ99964;

25-JUL-2000 (first entry)

DNA encoding a human osteoprotegerin ligand (OPGL).

Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

tumour necrosis factor receptor; type II transmembrane protein;

immune response; osteoporosis; bone resorption; ss.

Homo sapiens.

Location/Qualifiers

185..1138
/*tag= a
/product= "osteoprotegerin ligand"

W0200015807-A1.

23-MAR-2000.

13-SEP-1999; 99WO-DK00481.

15-SEP-1998; 98DK-0001164.

02-OCT-1998; 98US-0102896.

(MEBI-) M & E BIOTECH AS.

Haikier T, Haaning J;

WP: 2000-271444/23.

P-PSDB; AAY84417.

In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used

to treat, prevent and ameliorate osteoporosis -

Disclosure: Page 75-77; 110pp; English.

The present sequence encodes a human osteoprotegerin ligand (OPGL).

Osteoprotegerin is a secreted member of the tumour necrosis factor

receptor family, which blocks osteoclastogenesis in a dose dependent

manner. The OPGL protein is synthesised as a type II transmembrane

protein. The murine and human OPGL polypeptides are 87% homologous. OPGL

is a potent osteoclast differentiation factor when combined with CSF-1.

It is not capable of inducing osteoclast differentiation in the absence

of CSF-1. OPGL is also an activator of mature osteoclasts. The

specification describes a method for the in vivo down-regulation of

OPGL activity in an animal. The method comprises using at least one OPGL

polypeptide or subsequence, and/or at least one OPGL analogue to induce

an immune response in the animal. The method and OPGL polypeptide are

useful for treating, preventing and ameliorating osteoporosis or other

diseases or conditions characterised by excessive bone resorption.

Sequence 2271 BP; 658 A; 462 C; 522 G; 629 T; 0 other:

Query Match 100.0%; Score 954; DB 21; Length 2271;
Best Local Similarity 100.0%; Pred. No. 7.1e-241;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCCGCGCCAGACAGACATACACCAAGTACCTGCTGCTCGAGAGATGGCGGC 60
1 atggccgcgcagacagagactacacaaagctcgtgctcgagagatggcggc 60
185 atggccgcgcagacagagagactacacaaagctcgtgctcgagagatggcggc 244
61 GGGCCGGAGCCCGGACAGAGAGGCCCTCGACGCCCGCCGCTGGCGCCGACGAG 120
61 gggccggagcccgacagagagccctcgacgcccgccgctggcgccgacgag 120
245 gggccggagcccgacagagagccctcgacgcccgccgctggcgccgacgag 304

| | | | |
|----|------|---|------|
| OY | 121 | CCGCCCCGCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTT | 180 |
| OY | 122 | CCCCCGCGCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTT | 180 |
| Db | 305 | CCCCCGCGCGCTCCCGCTCCATGTTGCTGGCCCTCCTGGGGCTGGGGCTT | 364 |
| OY | 181 | GTCCTCAGCGTCGCGCCCTGTTCTTCTATTTTCAGACGCGAGATGGATGCTTATACAAATATCA | 240 |
| Db | 365 | gctctcagcgctcgccctgcttctctatcttcagcgcgagatgtaaccttaataataatca | 424 |
| OY | 241 | GAAGTGGCACTCACTGCATTTTATAGAAATTTTGAGACTCCATGAAAATGCAGATTTTTCAA | 300 |
| Db | 425 | gaagaatggcaactcactgcattctatagaattcttgagactccatgaaaatgagatttccaa | 484 |
| OY | 301 | GACACAACTCTCGAGAGCAAGATACAAAATTTATACCCTGATTCATGTCAGTACAGAAATTA | 360 |
| Db | 485 | gacacaactctgagagagatcacaagaatacaaaatcaataccgattctcatgtaggaataataa | 544 |
| OY | 361 | CAGGCTTTTCAAGAGAGCTGTGTCAAAAGAAATTTACAAATATCGTTGGATACAGCAATC | 420 |
| Db | 545 | cagggcttctcaagagagctgtgcaaaaggaattcaacaatatcgcttgatcacagccatc | 604 |
| OY | 421 | AGACGAGAAAGCGATGTGTGATGGCTCATGTTAGATGTGGCCAAAGACCAAGCTT | 480 |
| Db | 605 | agagagagaaagcgaatgtgtgagctgtctatgatactgtgcagaagagcaagctt | 664 |
| OY | 481 | GAAGCTCAGCCTTTTGGCATCTCATTATTAATGCGACGCAACATGCCATCTGGTTCCCAT | 540 |
| Db | 665 | gaagctcagcccttctgtcatctcaaccattaaatgcccgcgaatcccatctgttcccat | 724 |
| OY | 541 | AAAGTGAAGTCTGCTCTTGGTACCATGATCGGGGTGGGCAAGATCTCCAAATGACAT | 600 |
| Db | 725 | aaagtgaatctgtccctcttggtaaccatgtatcggggttgggccaagatctcccaatgact | 784 |
| OY | 601 | TTTATGCAATGGAACCTAATATAGTTAATCAGAGATGGCTTTATTAAGTGTATGCCAACAT | 660 |
| Db | 785 | tttatgcaatggaaaacctaatagtataaacaggaatggtcttattacatctgtatgccaaact | 844 |
| OY | 661 | TGCTTTGCACATCATGTGAACCTTCAGAGACCTAGCTACAGAGATATTTCAACTAATGGTG | 720 |
| Db | 845 | tgcttctgacatcatatgaacttccagggagacctagctacagagatcttccaactaatgtgtg | 904 |
| OY | 721 | TACCTCACTAAACACACATCAAAATCCCAAGTTTCATACCTGATGGAAGAGAGAAC | 780 |
| Db | 905 | tacgtccataaaacacacatcaataaattcccagttctcatatccctgtatgaagagagaagc | 964 |
| OY | 781 | ACCAAGATATTGGTCAGGCAATTTCTGAATTCATTTTATTTCCATTAAGCTGTGGGATTT | 840 |
| Db | 965 | accaagatattgtgtcaggaatcttgaaatctcatattctataatcaatgaagctgtgtgattc | 1024 |
| OY | 841 | TTTAAATTAAGCTGTGAGAGAAATCAGCATGAGAGTCTCCAAACCCCTCTTACTAGAT | 900 |
| Db | 1025 | tttaagtataagctgtcgtgagagaaatcagatctgagcttccaaacccctctactgtat | 1088 |
| OY | 901 | CCGAGATCAGAGTGCACATCTTTGGGGCTTTTAAAGTTCGAGATATTAGATTGA | 954 |
| Db | 1085 | ccgagatcagagatgcacaataactcttgggctctttaaagttctcgagataatagattga | 1138 |

| RESULT | 7 |
|----------|--|
| AAV70285 | ID 7 AAV70285 standard; DNA; 2274 BP. |
| XX | |
| XX | AAV70285: |
| AC | |
| XX | 11-FEB-1999 (first entry) |
| DT | |
| XX | |
| DE | Human osteoprotegerin binding protein from the pcDNA/huOPGp1.1insert. |
| XX | |
| KW | Human; osteoprotegerin binding protein; OPG binding protein; arthritis |
| KW | osteoporosis; osteoclast maturation; bone disease; metastasis; OPG; |
| KW | hypercalcaemia; osteoclast differentiation and activation receptor; |
| KW | Paget's disease; ss. |
| XX | |
| XX | |
| OS | Homo sapiens. |

| | | |
|----|---|-----------------------------------|
| XX | Key | Location/Qualifiers |
| FH | CDS | 185..1138 |
| FT | /*tag= | a |
| FT | /product= | "osteoprotegerin binding protein" |
| XX | | |
| XX | W09846751-A1. | |
| XX | | |
| XX | 22-OCT-1998. | |
| XX | | |
| XX | 15-APR-1998; | 98WO-US07584. |
| XX | | |
| XX | 30-MAR-1998; | 98US-0052521. |
| PR | 16-APR-1997; | 97US-0842842. |
| PR | 23-JUN-1997; | 97US-0880855. |
| XX | | |
| PA | (AMGE-) AMGEN INC. | |
| PI | Boyle WJ; | |
| XX | | |
| XX | WPI: 1998-594578/50. | |
| DR | P-PSDB; AAM83195. | |
| XX | | |
| PT | Nucleic acid encoding osteoprotegerin binding protein - useful for, | |
| PT | e.g. treating bone diseases by modulating osteoclast differentiation | |
| PT | and for diagnosis | |
| XX | | |
| PS | Claim 1; Fig 4; 47pp: English. | |
| XX | | |
| CC | The present sequence encodes human osteoprotegerin (OPG) binding protein. | |
| CC | Host cells transfected with vectors containing nucleic acid molecules | |
| CC | encoding OPG binding protein are used to produce recombinant OPG binding | |
| CC | protein. OPG binding protein is used in binding assays to determine | |
| CC | osteoprotegerin (OG) in biological samples; to screen for specific | |
| CC | binding agents (particularly agonists and antagonists, including | |
| CC | intracellular proteins); to raise Ab (useful in immunoassays for | |
| CC | detection of OPG binding protein) and to identify compounds that | |
| CC | modulate binding of OPG binding protein to osteoclast differentiation | |
| CC | and activator receptor (ODAR). The nucleic acid molecule encoding OPG | |
| CC | binding protein can be used to detect OPG binding protein-encoding | |
| CC | sequences, e.g. screening for related sequences, also to produce | |
| CC | transgenic animal models, while complementary sequences are used for | |
| CC | antisense regulation of OPG binding protein expression. Modulators of | |
| CC | OPG binding protein, particularly soluble forms of OPG binding protein | |
| CC | or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, | |
| CC | bone loss caused by arthritis or metastases, hypercalcaemia, Paget's | |
| CC | disease, periodontal disease, osteoporosis, loosening of prostheses, | |
| CC | optionally in combination with agents that promote bone growth. | |
| XX | | |
| XX | Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other: | |

| | | | | |
|-----------------------|----------------|---|----------|-------------|
| Query Match | 100.0% | Score 954 | DB 19 | Length 2274 |
| Best Local Similarity | 100.0% | Pred. No. 7 | Le-241 | |
| Matches 954 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | ATGCGCCGCGCAGCAGACATACACCAAGTACCTGCGTGCCTCGAGAGATGGCGGC | 60 | |
| Db | 185 | atgcgcgcgcgcagagagactacacacagatccctcgctgctcgagagatggcggc | 244 | |
| QY | 61 | GGCCCCGAGGCCCCGACAGAGGGCCCCCTGCACGCCCCCGCCGCTGCGCCACACAG | 120 | |
| Db | 245 | ggccccggagccccgcacagagggcccccttgacgccccgcgcgcctgcgcgcacag | 304 | |
| QY | 121 | CCCCCGCGGCTCCCGCTCCATGTTCTGTGGGCTCTGTGGGCTGGGGCTGGGCGAGTT | 180 | |
| Db | 305 | ccccccgcgcctccgcgtccalcgltgctgagccctccctcgggcgctggggccaggtc | 364 | |
| QY | 181 | GTCGACACGTCGCGCTGTTCTTCAATTTCAGAGCGCAGATGATCTCAATAGAATATCA | 240 | |
| Db | 365 | gtcgcgcagcgcctgcgcgtctctccatcttcagagcgagatggaccctaaatagaatcca | 424 | |
| QY | 241 | GAGATGGCACTCACTGATTTATAGAAATTTTGAGACCTCCATGAAATAAGCAGATTTTCA | 300 | |

```

Db      425 |||||||
Oy      301 GACGCAACTGTGAGAGCAAGATACAAATTAATACCTGATTGATGAGAGATTAAA 360
Db      485 gacacaactctggagagcgaagatacaaaaataactgttcatgttaggagattaaa 544
Oy      361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGAAATTACAACTATTCGTTGGATCAGACATC 420
Db      545 caggtcttcaaggagcgtgcaaaagaaattacaacatacgttgcacacacacalc 604
Oy      421 AGAGCAGAGAAAGGATGATGGATGGCTCATGTTAGATGCGCCAAAGAGAGCAAGCTT 480
Db      605 agagcagaagaagcgaigtggaigggccacaggttagatcggccaaaggaagcagctt 664
Oy      481 GAAGCTCAGCCCTTTGTCATCTCATTATTAATGCGCACGAGATCCATCTGTTCCCAT 540
Db      665 gaagctcagcctttgtccatctcacttaatgacacgcagatcccatctggtcccat 724
Oy      541 AAAGTACGCTGTGCTCTTGGTACCATGATCGGGGTTGGCCAGATCTCCAACTGACT 600
Db      725 aaagtgagctgtccctctgtgacatgatcggggttggtgccaagatctcaacalgact 784
Oy      601 TTTAGCAATGGAATACTAATAGTATAGATGAGATGCGCTTTTATTACCTGATGCCAAT 660
Db      785 tttagcaatgaaaaactaatgattatcaagatgagcttttattaccgttagccacact 844
Oy      661 TGCTTTGCATCATGAAATCTTCAGAGAGACTAGCTACAGAGATATCTTCACTAATGCTG 720
Db      845 tgccttcgcatcatgaagaaactcagagagaccagctacagagttacttcaactaagtgtg 904
Oy      721 TACGTCACATAAAGCAGATCAAAATCCCAATGCTCATACCTGATGATAAGAGAGAGAGC 780
Db      905 taagtcacaaacacagcaccacaaatcccaagttctcataccctgataaggaaggaagc 964
Oy      781 ACCAAGTATTTGGTCAGGGAATTCGAAATTCATTTTATTCATTAACGTTGGTGATTT 840
Db      965 accaagtatgtgcagggagattctgattcatttattcatalaagcgtgtgattt 1024
Oy      841 TTTTAAGTACGGCTCTGAGAGAGAAATCAGCATCGAGGTCCACACCCCTCTACTGAT 900
Db      1025 tttaagttacggtctgagagaaatcagcatcgaggtctccaaccccttacttgat 1084
Oy      901 CCGGATCAGGATGCAACATCTTTGGGGCTTTTAAAGTTCGAGATATAGATTGA 954
Db      1085 ccgagtcagagatgacaacactttg99gctttaaagttcagagataagattga 1138

RESULT      8
AAV69887
ID      AAV69887 standard; cDNA to mRNA; 954 BP.
AC      AAV69887;
DT      10-FEB-1999 (first entry)
XX      Nucleic acid encoding a human OCIF-binding molecule (OBM).
XX      DE
XX      XX
XX      Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
XX      KW osteoclast; bone absorption factor; Bone disorder; calcium metabolism;
XX      KW human; ss.
XX      OS
XX      Homo sapiens.
XX      FH
XX      Key Location/Qualifiers
XX      FT 1..954
XX      FT CDS /tag= a
XX      PN
XX      MO9846644-A1.
XX      PD 22-OCT-1998.
XX      PF 15-APR-1998; 98WO-JP01728.

```

```

XX      02-DEC-1997; 97JP-0332241.
PR      15-APR-1997; 97JP-0097808.
PR      09-JUN-1997; 97JP-0151434.
PR      12-AUG-1997; 97JP-0217897.
PR      21-AUG-1997; 97JP-0224803.
XX      (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA      Goto M, Hiasashio K, Kinoshaki M, Kobayashi F, Morinaga T;
PI      Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI      Washida N, Yamaguchi K, Yano K, Yasuda H;
XX      WPI: 1998-594563/50.
DR      P-PSDB; AAM83018.
XX      Protein binding to osteoclastogenesis inhibitory factor - useful
PT      for, e.g. treatment and investigation of disorders of bone and
PT      calcium metabolism
XX      Claim 38; Page 115; 151pp; Japanese.
PS      The present sequence encodes an osteoclastogenesis inhibitory factor
CC      (OCIF)-binding molecule (OBM). The protein promotes and supports the
CC      separation and maturation of osteoclasts in the presence of bone
CC      absorption factors such as calcitriol or parathyroid hormone (PTH).
CC      OBM is isolated from stroma cells cultured in the presence of a bone
CC      absorption factor by separation using OCIF. It exists in a full-sequence
CC      then affinity chromatography using OCIF. It is a shorter chain. OBM may be
CC      form and a solubilised form (SOBM) which is a shorter chain. OBM may be
CC      used for screening potential inhibitors and modulators of its functional
CC      activity, and screening for receptors to OBM which mediate its function.
CC      These substances can then be used in the treatment of disorders of bone
CC      function and calcium metabolism. The antibodies can be used for assay
CC      of the protein, for investigative and diagnostic purposes, and as
CC      components of drugs.
XX      Sequence 954 BP; 255 A; 239 C; 226 G; 234 T; 0 other;
SQ

Query Match      99.7%; Score 950.8; DB 19; Length 954;
Best Local Similarity 99.8%; Pred. No. 3; 5e-240;
Matches 952; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 ATGCGCGCGCGCAGCAGAGACTACACCAAGTACCTGCTGCTCGAGAGATGGCGGC 60
Db      1 atgcgcgcgccagagagactaacacaaagtacctgctgctcgagagatgagcgc 60
Oy      61 GCGCCCGAGGCCCGCAGAGAGGGCCCTCGACGCGCCGCGCGCGCGCGAGCAG 120
Db      61 ggcgccgagccccgcagagagcgccccctgacgccccgcgcgcgcgcgcgcag 120
Oy      121 CCGCCCGCGCGCTCCGCGCTCATGTTCTGTGGCCCTCTGTGGGGCTGGGGCCAGGTT 180
Db      121 cccctgcgcgctcccgctccatgttctgtgcccctccggggcctgaggccaggtt 180
Oy      181 GTCTCAGCGTGGCCCTGTTCTTATTTACAGCGCGAGATGATCTTAATGAATATCA 240
Db      181 gtctcagcgctgcccctgttcttcatctcagagcgagatgagatcacaataagatca 240
Oy      241 GAAGATGGACACACTGCAATTTATAGAAATTTGACATTCATGAAATGAGATTTCAA 300
Db      241 gaagatggacacactgcaatttataagaaatttgagatccatgaaaatgcaagatttcaa 300
Oy      241 gaagatggaactcaactgcatctatagaaatttgagatccatgaaaatgcaagatttcaa 300
Db      301 GACACAATCTGTGAGAGTCAAGATCAAAATTAATACCTGATTTCATGTAGGAATTAAA 360
Oy      301 gacacaactctgagagtgtaagatacaaaaataactaactgattcatgttaggaattaaa 360
Db      361 CAGGCTTTCAAGAGAGCTGTGCAAAAAGAAATTACAACTATTCGTTGGATCAGACATC 420
Oy      361 caggtcttcaaggagcgtgcaaaagaaattacaacatacgttgcacacacalc 420
Db      421 AGAGCAGAGAAAGGATGATGGATGGCTCATGTTAGATGCGCCAAAGAGAGCAAGCTT 480

```



```
|||||
Db 601 ttltatccataaacgttggatgttttaagtacggtcgcgaggaatcagcacc 660
QY 874 GAGGCTCCACACCCCTCTTACTGATCGATCGATGCAACATACCTTTGGGCTTTT 933
Db 661 gaggctcccaaccctccttactgataccgatacgatgcacactacttggggctt 720
QY 934 AAAGTTGAGATATAGATTGA 954
Db 721 aaagtcgagatatagattga 741

RESULT 10
AA80223
ID AA80223 standard; cDNA; 1823 BP.
AC AA80223;
XX 17-AUG-1999 (first entry)
DE Human TRANCE encoding cDNA.
XX
XX TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
XX TNF-related activation induced cytokine; immune response; cancer;
XX autoimmune disease; HIV; hypersensitivity; allergen; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..738
FT /*tag= a
PN WO929865-A2.
XX 17-JUN-1999.
PD 14-DEC-1998; 98WO-US26486.
XX 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1998; 98US-0034099.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
PA Choi Y, Josien R, Steinman R, Won B;
PI WPI; 1999-385609/32.
DR P-PSDB; AAY17873.
XX
XX TNF like proteins for treating autoimmunity and cancer
PT Claim 1; Fig 1; 164pp; English.
XX
XX The present sequence encodes human TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising: antisense sequences to
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX Agonists and antagonists of TRANCE, can be used to modulate immune
XX response by increasing or decreasing the life span of mature dendritic
XX cells and increasing or decreasing T cell activation. These techniques
XX are especially useful for treating immune system related conditions such
XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX The TRANCE polypeptides can be used to increase the viability of
XX dendritic cells in vivo or in vitro, especially when used in conjunction
XX with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CD40L or TNF-alpha).
XX
XX Sequence 1823 BP; 569 A; 305 C; 380 G; 569 T; 0 other;

Query Match 76.9%; Score 733.2; DB 20; Length 1823;
Best Local Similarity 99.6%; Pred. No. 8e-183;
```

```
Matches 735; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 217 CAGATGATCCTTAATAGAAATATGCAAGATGGCACTCAGCAATTATAGAAATTTTGA 276
Db 1 cagatgatacctaataaatacagaagatgacatcagcatcttataaatttgaga 60
QY 277 CTCGATGAAATGCGAGATTTTCAAGACACAACCTGAGAGTCAAGATACAAAATTAATA 336
Db 61 ctccatgaaatgcatgatttccaagacacactctgagatgaagtatacaaatata 120
QY 337 CCGATTCATGTAGAGAAATTAACAGGCGCTTTTAAGAGAGCTGTCGCAAAAGAAATTCAA 396
Db 121 cctgattcatgtagagaaatlaaacagcccttlaaagagcctgycaaagaaatlaaa 180
QY 397 CATATCGTTGATCATACACATCATCAGACAGAGAAAGAGATGTGATGGCTCATGTGTTA 456
Db 181 catatcgttggatacagacacatcagacagaaagagatggtggtcctatggtta 240
QY 457 GATCTGGCCAAAGAGAGAGCAAGCTTGAAGCTCAGGCTTTTGCTCATCTATTATGCC 516
Db 241 gatctggccaagagagagcaagcttgaagctcagccttltgctcatcactataatgyc 300
QY 517 ACCGACATCCCATCTGCTTCCCATTAAGTGAAGTCTGCTCCTTGATACATGCGGGT 576
Db 301 accgacatcccatctgcttccataaagtgagctgctccttggtaaccatgacgcgggg 360
QY 577 TGGGCCAAGATCTCCAAATGACTTTTAGCAATGGAAGAAATTAATAGTTAATCAGATGCC 636
Db 361 tggggtaagatctccaatgacttlttagcaatggaataactaagtatcagatgag 420
QY 637 TTTTATTAACCTGTATGCCAACATTTGCTTTCGACATCATGAATCTTACGAGACCTAGCT 696
Db 421 ttltatccgtttagccaacatttgccttcgacatcatgaactcagagacttagct 480
QY 697 ACAGAGATACCTTCACACTATATGCTAGCGTCACTAAACAGACATCAAAATCCAACTCT 756
Db 481 acagagatcttcaactaatgltgtagtcactaaacagacataaataccaaagttct 540
QY 757 CATACCTGATGAAGAGAGAGACCAAGTATTTGGTCAGGGAATTCGAATTCATTTT 816
Db 541 cataccctgataaagagagagacccaagatltgtagggaattcgaattccattt 600
QY 817 TATTCATTAACGTTGGTGGATTTTAAAGTTACGCTCTGGAGAGGAATACGATCGAG 876
Db 601 tatccataaacgttggatgttttlaagtlacggtctgagaggaatcaagcatcgag 660
QY 877 GGTCCCAACCCGCTTACTGATCGATCGATGCAACATACCTTTGGGCTTTTAAA 936
Db 661 gtcccaaccctccttactgataccgatacgatgcacatacttggggctttaa 720
QY 937 GTTCGAGATATAGATTGA 954
Db 721 gtctgagatatagattga 738

RESULT 11
AAF86481
ID AAF86481 standard; cDNA; 957 BP.
XX
XX AAF86481;
XX 29-JUN-2001 (first entry)
XX
XX Rat osteoclast differentiation factor, ODF, coding sequence.
XX
XX Rat; osteoclast formation inducer; vaccine; gene therapy;
XX Osteoclast Differentiation Factor; bone; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
FH CDS 1..957
FT /*tag= a
```



```

OY 1 ATGCGCGCGCCAGACAGACTACCAAGTACTGCTGGCTGGAGAGAGATGGCGGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgagcgagcgagcgagcgagtaacgtaactgctgagcgagctgagagatgagcgagc 60
OY 61 GGCCCCGGAGCGCCGCAAGAGAGGCCCCCTGCACGCCCGCCG---GGCGCCCTGGCCGCGAC 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ggcgcgagcgagcgagcgagagggctgcagcccgagctctgtcagcgagcgagcgagc 120
OY 118 CAGCCCCCGCGCGCTCCGCTCATGTTTCGTGGCCCTCCCTGGGGCTGGGGCTGGGCGAG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 cgcgcaacgcgcgcctccgcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 180
OY 178 GTTGTCTGCAGCGTCCGCTGCTTCTTATTTTCAGAGCGAGATGATCTTAATAGATA 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gtggtctgcagcagctgctctcctcctcctcctcctcctcctcctcctcctcctcctc 240
OY 238 TCAGAGATGGCACTCACTGATTTATAGATTTTGAAGTCCATGAAATGAGATTTT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 tcagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
OY 298 CAGACACAACTGTGAGAGTCAAGATACAAATTAATACCTGATTCATGTAGAGATA 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 cagagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 354
OY 358 AACACAGCGCTTTCAAGAGCTGTCCAAAGAGATTTACACATATCTGTGATCACAGCAC 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 aaaaacagccttcagagggcgctgcaagaggaactgcaacacatctgagggccacagcgc 414
OY 418 ATCAGACAGAGAAAGGATGGATGGCATGATGATGATGATGATGATGATGATGATGAT 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 ttcacagagagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 474
OY 478 CTGGAAGCTCAGCGCTTTTGTCTCATCTATTAATGCGACGACATCCATCTGCTTCC 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 ccctgagcgccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 534
OY 538 CATTAAGTACTGTCTCTCTGTTGATCAGATGATGGGGTGGGCGCAAGATCCACATG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 cataaagtcacctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 594
OY 598 ACTTTTGGCAATGGAATACTAATAGATGATGATGATGATGATGATGATGATGATGAT 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 acgttaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 654
OY 658 ATTTGCTTTCAGCATGATGAATTTTCAGAGAGCTAGCTACAGATGATCTTCAACTAATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 attgccttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 714
OY 718 GTGATGCTACTAAACCCAGCATCAAAATCCCAAGTTCTCATACCTGTGATGAAGAGA 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 gtgtatgtcgttaaaacagcagcagcagcagcagcagcagcagcagcagcagcagc 774
OY 778 AGCACAAGTATTTGGTGAAGGAAATTCGAATTCATTTTATTCATTAAGCTGGTGA 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 775 agcgcaaaaacatgctgagcagcagcagcagcagcagcagcagcagcagcagcagc 834
OY 838 TTTTATGATTCAGTCTGAGAGAAATTCAGATCAGATCAGATCAGATCAGATCAGAT 897
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 835 ttttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 894
OY 898 GATCCGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 895 gatccgagtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 951

```

RESULT 14

AAZ99965 standard; DNA: 951 BP.

```

XX AAZ99965:
XX
XX
XX 25-JUL-2000 (first entry)
XX

```

```

DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..951
FT CDS
FT
FT /tag= a
FT /product= "osteoprotegerin ligand"
XX
Db W0200015807-A1.
XX
Db 23-MAR-2000.
XX
Db 13-SEP-1999; 99WO-DK00481.
XX
Db 15-SEP-1998; 98DK-0001164.
XX
Db 02-OCT-1998; 98US-0102896.
XX
Db (MEBI-) M & E BIOTECH AS.
XX
Db Halkier T, Haaning J;
XX
Db WPI: 2000-271444/23.
XX
Db P-PSDB; AAY84418.
XX
Pt In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
Pt to treat, prevent and ameliorate osteoporosis -
XX
Ps Disclosure; Page 79-81; 110pp; English.
XX
Cc The present sequence encodes a murine osteoprotegerin ligand (OPGL).
Cc Osteoprotegerin is a secreted member of the tumour necrosis factor
Cc receptor family, which blocks osteoclastogenesis in a dose dependent
Cc manner. The OPGL protein is synthesised as a type II transmembrane
Cc protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
Cc is a potent osteoclast differentiation factor when combined with CSF-1.
Cc It is not capable of inducing osteoclast differentiation in the absence
Cc of CSF-1. OPGL is also an activator of mature osteoclasts. The
Cc specification describes a method for the in vivo down-regulation of
Cc OPGL activity in an animal. The method comprises using at least one OPGL
Cc polypeptide or subsequence, and/or at least one OPGL analogue to induce
Cc an immune response in the animal. The method and OPGL polypeptide are
Cc useful for treating, preventing and ameliorating osteoporosis or other
Cc diseases or conditions characterised by excessive bone resorption.
XX
S0 Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other:

```

```

Query Match 69.8%; Score 666.2; DB 21; Length 951;
Best Local Similarity 82.5%; Pred. No. 2.0e-165;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

```

```

OY 1 ATGCGCGCGCCAGACAGACTACCAAGTACTGCTGGCTGGAGAGATGGCGGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgagcgagcgagcgagcgagtaacgtaactgctgagcgagctgagagatgagcgagc 60
OY 61 GGCCCCGGAGCGCCGCAAGAGAGGCCCCCTGCACGCCCGCCG---GGCGCCCTGGCCGCGAC 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ggcgcgagcgagcgagcgagagggctgcagcccgagctctgtcagcgagcgagcgagc 120
OY 118 CAGCCCCCGCGCGCTCCGCTCATGTTTCGTGGCCCTCCCTGGGGCTGGGGCTGGGCGAG 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 cgcgcaacgcgcgcctccgcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 180
OY 178 GTTGTCTGCAGCGTCCGCTGCTTCTTATTTTCAGAGCGAGATGATCTTAATAGATA 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gtggtctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 240

```

```
OY 238 TCAGAGATGGCACTCACTGATTATAGAAATTTGAGACTGCATGAATAATGCAGATT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 tcagaagacagactcactgtcttataagaaacctgaaacctcgaataaagcggtttg 300
OY 298 CAAGACAACTCTGGAGAGTCAAGATCAAAATTAATACCTGATTCATGTAGAGAAAT 357
    || || || || || || || || || || || || || || || || || || || || ||
Db 301 cagactcagactcgtgagagtgaaagacac-----actactgactcctcgtgagagtg 354
OY 358 AAAAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACAACTATCGTTGATTCACAGAC 417
    ||||| ||||| || || || || || || || || || || || || || || || || ||
Db 355 aaacaagccttcaggggcccgtgcgaagaaactgcacacatctgtggggccacagcgc 414
OY 418 ATCAGACAGAGAAAGGATGGTGGATGGCTCATGTAGATCTGGCCAAAGAGAGCAAG 477
    || || || || || || || || || || || || || || || || || || || || ||
Db 415 ttctcagagagctcagctatgatggaagcctcagtggtgtgtggccacagcgagcaag 474
OY 478 CTGGAAGCTCAGCTTTTGTCTCATCTCATTAATTAATGCGACGACATCCATCTGGTTC 537
    || || || || || || || || || || || || || || || || || || || || ||
Db 475 cctgagggccagcattgtcacacctcaccaatcgaatgtgcagacatcccatcggttcc 534
OY 538 CATAAAGTACTCTGCTCTCTTGTACCATGATGGGGTTGGGCAANATCTCCAACTG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 cataaagctactcgtccctctgtgacacagatcgagggcgcgaatcctcaaatg 594
OY 598 ACTTTAGCAATGGAACCTAATAGTATCAGATGGCTTTTATTAACCTGATGCGAAC 657
    || || || || || || || || || || || || || || || || || || || || ||
Db 595 acgttaagcaacggaataaactaaggttaacaaagatggtcttatctactgttaagccaac 654
OY 658 ATTTGCTTTGCATCATGAAACTTTCAGAGAGACTAGCTACAGATATCTTCAACTATG 717
    || || || || || || || || || || || || || || || || || || || || ||
Db 655 attgcttcgagcatcagaacacgcggagcgtlaactaagactacttcaactgtatg 714
OY 718 GTGAGCTCACTAAACACGATCAAAATCCCAAGTCTACCCATCATGAAAGAGAGA 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 gtgtatgctgataaaccagatcaaaatcccaagttctcaaacgtgaagaaagaggg 774
OY 778 AGCACAAGTATGTCAGGAAATTCGAATTCATTTTATTCATCAACGTTGGTGA 837
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 775 agcagaanaactgtgtgggcaattcgaattccactttatccataaatggttgagg 834
OY 838 TTTTAAAGTACGCTCTGGAGAGAAATCAGCATCGAGGCTCCAAACCTCCTTACTG 897
    ||||| || || || || || || || || || || || || || || || || || || ||
Db 835 ttctcgaagctccgagctggtgaaatctagcaltcagtggtccaaaccttcctgctg 894
OY 898 GATCGGATCGAGATGCAACATACTTGGGCTTTTAAAGTTCGAGATATGATTGA 954
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 895 gatccgatacagatgagcgtacttgggtgttcaaaagttcagagacatagactga 951
```

RESULT 15

```
AAZ49024
ID AAZ49024 standard; DNA; 951 BP.
XX
AC AAZ49024:
XX
DT 31-MAR-2000 (first entry)
XX
DE osteoclast formation promoting factor coding sequence.
XX
KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
KW bone metabolic disease; osteoporosis; therapy; ss.
XX
OS Mus sp.
XX
PN JP11332581-A.
XX
PD 07-DEC-1999.
XX
PF 20-OCT-1998; 98JP-0316973.
XX
PR 24-MAR-1998; 98JP-0076232.
XX
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
```

```
PA (SANY ) SANKYO CO LTD.
XX
DR WPI; 2000-091362/08.
XX
PT A new protein, a DNA and its application -
XX
PS Example 1; Page 13; 18pp; Japanese.
XX
CC This sequence encodes the osteoclast formation promoting factor (OBM-BP).
CC The invention relates to an OBM binding protein (OBM-BP). The protein is
CC useful as a preventive and/or treating agent for bone metabolic diseases
CC such as osteoporosis. Substances which inhibit the binding of OBM to
CC OBM-BP can be used as biochemical reagents.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
```

Query Match 69.8%; Score 666.2; DB 21; Length 951;
Best Local Similarity 82.5%; Pred. No. 2.6e-165;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

```
OY 1 ATGCGCCGCGCCAGCAGAGACTACACCAAGTACTGCTGGCTGGAGAGATGGGCGC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atgcgcggcgccagcagactacgcaagtaactcgtgcagctcgagagagatggcgagc 60
OY 61 GGCCCGGAGCCCGCAGAGAGGCGCCCTGCAGCGCCCGC---CGCGCCTGCGCGCGAC 117
    ||||| || || ||||| || || ||||| || || || || || || || || || || ||
Db 61 ggcgccggtgcctccacaagaaggtcgcgtgtcaccgccggtcttgcaacgcgtccgcgcg 120
OY 118 CAGCCCGCGCGCGCTCCGCTCATGTTGCTGGCCCTCTCTGGGCTGGGCTGGGCCAG 177
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ccgcacccgcgcctcccgctccatgttctcgtgcccctctggggctggagactgggcccag 180
OY 178 GTGCTGTCAGAGCTGCGCCCTGTCTTATTTTCAGAGCGAGATGAGATCTTAATAGAATA 237
    || ||||| || || ||||| || || || || || || ||||| ||||| ||||| |||||
Db 181 gtgtctgcagacatcgcgtgtctcgtacttcgaagcgagatcgatcccaacagaata 240
OY 238 TCAGAAAGTATGCACTCACTGATTTATAGAAATTTTGAGACTCATGAAATGCAGATT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 tcagaagcagcactcactcgtcttataagaaacctgaaacctcgaataaagcggtttg 300
OY 298 CAAGACAACTCTGGAGAGTCAAGATCAAAATTAATACCTGATTCATGTAGAGAAAT 357
    || || || ||||| ||||| || || ||||| || || ||||| || || ||||| || ||
Db 301 cagactcagactcgtgaaagtgaaagacac-----actactgactcctcgtgagagtg 354
OY 358 AAAAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACAACTATCGTTGATTCACAGAC 417
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 aaacaagccttcaggggcccgtgcgaagaaactgcacacatctgtggggccacagcgc 414
OY 418 ATCAGAGCAGAGAAAGGATGGTGGATGGCTCATGTAGATCTGGCCAAAGAGAGCAAG 477
    || || || || || || || || || || || || || || || || || || || || ||
Db 415 ttctcagagagctcagctatgatggaagcctcagtggtgtgtggccacagcgagcaag 474
OY 478 CTGGAAGCTCAGCTTTTGTCTCATCTCATTAATTAATGCGACGACATCCATCTGGTTC 537
    || || || || || || || || || || || || || || || || || || || || ||
Db 475 cctgagggccagcattgtcacacctcaccaatcgaatgtgcagacatcccatcggttcc 534
OY 538 CATAAAGTACTCTGCTCTCTTGTACCATGATGGGGTTGGGCAANATCTCCAACTG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 cataaagctactcgtccctctgtgacacagatcgagggctgtggccaaagatctcaaacg 594
OY 598 ACTTTAGCAATGGAACCTAATAGTATCAGATGGCTTTTATTAACCTGATGCGAAC 657
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 acgttaagcaacggaanaactaaggtttaaccaagtgtctctatctactgtaagccaac 654
OY 658 ATTTGCTTTGCATCATGAAACTTTCAGAGAGACTAGCTACAGATATCTTCAACTATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 attgcttcgagcatcagaacacgcggagcgtlaactaagactacttcaactgtatg 714
OY 718 GTGAGCTCACTAAACACGAGATCAAAATCCCAAGTCTCATGATCCGTTGAAAGAGAGA 777
    ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 gtgtatgctgataaaccagatcaaaatcccaagttctcaaacgtgaagaaagaggg 774
```

QY 778 AGACCAAGTATTGTCAGGAATTCTGAATTTTATTCATTAACGTTGGTGA 837
 Db 775 agcagcaaaacgcggtcgaatctgaaatccacttlatccaataatgttg999ga 834
 QY 838 TTTTAAAGTTACGTCAGAGAAATCAGATCAGAGTCTCCAAACCCCTCTACTG 897
 Db 835 ttttcaagctccgagctcgtagaataatgcatcagggtgccaaaccttccctgctg 894
 QY 898 GATCCGGAATCAGATCAACATACTTTGGGCTTTTAAAGTTGAGATATAGATTGA 954
 Db 895 gatccgaltcaagatgcgacgtacttcttg99gcttcaaaagttcagagacataagactga 951

Search completed: July 8, 2002, 21:43:51
 Job time: 6085 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2002, 20:04:31 ; Search time 96.15 Seconds
(without alignments)
2437.175 Million cell updates/sec

Title: US-09-865-363-12

Perfect score: 954

Sequence: 1 ATGCGCCGCCGACAGAGA.....AAGTTCAGATATGATTGA 954

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/1na/PCRN.COMB.seq:*

6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------------|
| 1 | 954 | 100.0 | 954 | 3 | US-08-996-139-12 |
| 2 | 954 | 100.0 | 954 | 4 | US-08-995-659-12 |
| 3 | 954 | 100.0 | 954 | 4 | US-09-215-649A-12 |
| 4 | 954 | 100.0 | 2271 | 4 | US-09-052-521C-3 |
| 5 | 666.2 | 69.8 | 2191 | 4 | US-08-989-362-1 |
| 6 | 666.2 | 69.8 | 2295 | 2 | US-08-842-842-6 |
| 7 | 666.2 | 69.8 | 2295 | 4 | US-09-052-521C-1 |
| 8 | 615 | 64.5 | 1630 | 3 | US-08-996-139-10 |
| 9 | 615 | 64.5 | 1630 | 4 | US-08-995-659-10 |
| 10 | 615 | 64.5 | 1630 | 4 | US-09-215-649A-10 |
| 11 | 69.4 | 7.3 | 759 | 4 | US-09-320-424-12 |
| 12 | 69.4 | 7.3 | 759 | 4 | US-09-320-424-10 |
| 13 | 69.4 | 7.3 | 1042 | 3 | US-08-584-031-2 |
| 14 | 69.4 | 7.3 | 1042 | 3 | US-08-780-486-2 |
| 15 | 69.4 | 7.3 | 1521 | 1 | US-08-670-354-3 |
| 16 | 69.4 | 7.3 | 1521 | 4 | US-09-320-424-3 |
| 17 | 69.4 | 7.3 | 1521 | 5 | PCT-US96-10895-3 |
| 18 | 69.4 | 7.3 | 1751 | 1 | US-08-670-354-1 |
| 19 | 69.4 | 7.3 | 1751 | 4 | US-09-320-424-1 |
| 20 | 69.4 | 7.3 | 1751 | 5 | PCT-US96-10895-1 |
| 21 | 69.4 | 7.3 | 1769 | 4 | US-09-333-593A-5 |
| 22 | 69.4 | 7.3 | 1769 | 4 | US-09-505-250-1 |
| 23 | 57.6 | 6.0 | 1366 | 1 | US-08-670-354-5 |
| 24 | 57.6 | 6.0 | 1366 | 4 | US-09-320-424-5 |
| 25 | 57.6 | 6.0 | 1366 | 5 | PCT-US96-10895-5 |
| 26 | 41.8 | 4.4 | 15331 | 3 | US-09-128-155-16 |
| 27 | 41.4 | 4.3 | 1777 | 1 | US-08-173-508-5 |

| | | | | | | |
|----|------|-----|-------|---|------------------|-------------------|
| 28 | 41.4 | 4.3 | 1777 | 2 | US-08-265-310-5 | Sequence 5, Appl |
| 29 | 41.4 | 4.3 | 1777 | 2 | US-08-951-742-5 | Sequence 5, Appl |
| 30 | 40.6 | 4.3 | 44377 | 2 | US-08-804-227C-7 | Sequence 7, Appl |
| 31 | 40.6 | 4.3 | 44377 | 2 | US-08-804-186-1 | Sequence 1, Appl |
| 32 | 40 | 4.2 | 2000 | 4 | US-08-426-509A-1 | Sequence 1, Appl |
| 33 | 40 | 4.2 | 2000 | 5 | PCT-US95-05008-1 | Sequence 1, Appl |
| 34 | 40 | 4.2 | 30001 | 1 | US-08-125-468-1 | Sequence 1, Appl |
| 35 | 40 | 4.2 | 30001 | 2 | US-08-474-933-1 | Sequence 1, Appl |
| 36 | 39.4 | 4.1 | 4451 | 3 | US-08-717-284-42 | Sequence 42, Appl |
| 37 | 39.2 | 4.1 | 5474 | 4 | US-09-040-738-1 | Sequence 1, Appl |
| 38 | 39.2 | 4.1 | 5474 | 4 | US-08-652-426A-1 | Sequence 1, Appl |
| 39 | 39 | 4.1 | 1853 | 4 | US-08-952-061-1 | Sequence 1, Appl |
| 40 | 38.8 | 4.1 | 1485 | 1 | US-08-471-601-23 | Sequence 23, Appl |
| 41 | 38.8 | 4.1 | 1485 | 1 | US-08-474-556-23 | Sequence 23, Appl |
| 42 | 38.8 | 4.1 | 1485 | 1 | US-08-479-382-23 | Sequence 23, Appl |
| 43 | 38.8 | 4.1 | 1485 | 1 | US-08-470-354-23 | Sequence 23, Appl |
| 44 | 38.8 | 4.1 | 1485 | 1 | US-08-479-383-23 | Sequence 23, Appl |
| 45 | 38.8 | 4.1 | 1485 | 2 | US-08-479-041-23 | Sequence 23, Appl |

ALIGNMENTS

RESULT 1
US-08-996-139-12
Sequence 12, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 954 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE: huRANKL (full length)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..951
US-08-995-139-12

Query Match 100.0%; Score 954; DB 3; Length 954;
Best Local Similarity 100.0%; Pred. No. 2.5e-251;
Matches 954; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGCGCGCGCAGAGACTACACCAAGTACTGCTGCTCGGAGAGATGGCGGC 60
DB 1 ATGCGCGCGCGCAGAGACTACACCAAGTACTGCTGCTCGGAGAGATGGCGGC 60

QY 61 GGGCCCGAGAGCCCGCAGAGAGGGGCCCTGCAAGCCCGCGCGCTGCGCGCACAG 120
DB 61 GGGCCCGAGAGCCCGCAGAGAGGGGCCCTGCAAGCCCGCGCGCTGCGCGCACAG 120

QY 121 CCCCCCGCGCGCTCCCGCTCCATGTTGCTGCGGCTCGGGGCTGGGGCCAGGTT 180
DB 121 CCCCCCGCGCGCTCCCGCTCCATGTTGCTGCGGCTCGGGGCTGGGGCCAGGTT 180

QY 181 GTCGTGAGCGTGGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATGAAATATCA 240
DB 181 GTCGTGAGCGTGGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATGAAATATCA 240

QY 241 GAAAGTGGCAGCTCAGCTGCTTTATAGAAATTTGAGACTCCATGAAATGCAATTTTCAA 300
DB 241 GAAAGTGGCAGCTCAGCTGCTTTATAGAAATTTGAGACTCCATGAAATGCAATTTTCAA 300

QY 301 GACACAACTCTGGAGAGTCAAGATACAAATTAATCTGATTCATGTGAGAAATTTAA 360
DB 301 GACACAACTCTGGAGAGTCAAGATACAAATTAATCTGATTCATGTGAGAAATTTAA 360

QY 361 CAGGCGCTTTCAGAGAGCTGTGCAAAAGAAATTACAACATATCGTTGGATCAGACACATC 420
DB 361 CAGGCGCTTTCAGAGAGCTGTGCAAAAGAAATTACAACATATCGTTGGATCAGACACATC 420

QY 421 AGAGCAGAGAAAGCGATGCTGATGCTCATGCTATGCTGGCCAAAGAGGAGCAAGCTT 480
DB 421 AGAGCAGAGAAAGCGATGCTGATGCTCATGCTATGCTGGCCAAAGAGGAGCAAGCTT 480

QY 481 GAAAGTCAAGCTTTTGTCTCATCTCACTATTAAATGCCAGGACATCCCATCTGGTCCCAT 540
DB 481 GAAAGTCAAGCTTTTGTCTCATCTCACTATTAAATGCCAGGACATCCCATCTGGTCCCAT 540

QY 541 AAGTGAAGTCTGCTCTGTTGATACATGATCGGGGTTGGGCCAAGATCTCCAAATGACT 600
DB 541 AAGTGAAGTCTGCTCTGTTGATACATGATCGGGGTTGGGCCAAGATCTCCAAATGACT 600

QY 601 TTTAGCAATGGAAACTAATAGTTAATCAGAGTGGCTTTTATTAAGTGTGCAACATT 660
DB 601 TTTAGCAATGGAAACTAATAGTTAATCAGAGTGGCTTTTATTAAGTGTGCAACATT 660

QY 661 TGGCTTCGACATCATGAAACTTCAGAGAGACTAGTACAGAGATATCTCAACTAATGATG 720
DB 661 TGGCTTCGACATCATGAAACTTCAGAGAGACTAGTACAGAGATATCTCAACTAATGATG 720

QY 721 TACGTACTATAAACAAGCATCAAAATCCCAAGTTCATACCTGATGAAAGAGAGAGC 780
DB 721 TACGTACTATAAACAAGCATCAAAATCCCAAGTTCATACCTGATGAAAGAGAGAGC 780

QY 781 ACCAATATTTGTCAGAGAAATCTGAATCCATTTTATTCATTAACGTTGGTGGATTT 840
DB 781 ACCAATATTTGTCAGAGAAATCTGAATCCATTTTATTCATTAACGTTGGTGGATTT 840

QY 841 TTTAAGTTACGTCGTGAGAGAAATCAGATCAGGATCTCCAAACCCCTTACTGAT 900

DB 841 TTTAAGTTACGTCGTGAGAGAGAAATCAGATCAGGATCTCCAAACCCCTTACTGAT 900
QY 901 CCGGATCAGGATGACAACATACTTTGGGCTTTTAAAGTTCCAGATATGATTTGA 954
DB 901 CCGGATCAGGATGACAACATACTTTGGGCTTTTAAAGTTCCAGATATGATTTGA 954

RESULT 2
US-08-995-659-12
; Sequence 12, Application US/0895659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Gallibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 954 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: huRANKL (full length)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
US-08-995-659-12


```
RESULT 5
US-08-989-362-1
; Sequence 1, Application US/08989362
; Patent No. 6242586
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Meltson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: DNA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 125..1072
US-08-989-362-1

Query Match 69.8%; Score 666.2; DB 4; Length 2191;
Best Local Similarity 82.5%; Pred. No. 1.5e-172;
Matches 790: Conservative 0; Mismatches 158; Indels 9; Gaps 2;
```

```
Db 365 TCAGAGACAGACGCTCAGCTTTTATAGATCCTGAGACCTCATGAAACGACGTTTG 424
Qy 298 CAAGACACACTCTGGAGAGTCAAGATACAAATTAATACCTGATTATGTAGAGAAAT 357
Db 425 CAGACCTGACCTCTGAGAGTGAAGACAC-----ACTACCTGACTCTGACGAGGATG 478
Qy 358 AAACAGGCTTTCAAGAGCTGTGCAAAAGAAATTAACAATATGCTTGATCAACAGC 417
Db 479 AAACAAGCTTTCAAGAGGCGCTGCAAGAGAACTGCAACATTTGTGGGCGACAGCGC 538
Qy 418 ATCAGACAGAGAAAGCAGATGTGATGAGCTCATGATTAGATCTGCGCAAGAGAGCAAG 477
Db 539 TTCTCAGAGAGCTCCAGCTATGATGGAAGGCTCATGTTGATGTTGGCCAGAGGCAAG 598
Qy 478 CTTGAAGCTCAAGCTTTTGTCTCATCTCATATTATGCGACGAGATCCCATCTGTTCC 537
Db 599 CCGTAGGCGCCAGCATTTGCAACCTCAACATCAATGTGCGCAGCATCCATCGGGTTC 658
Qy 538 CATTAAGTAGTCTGCTCTTGTGATCAGATGATCGGGGTGGGCCAAGATCCCAATG 597
Db 659 CATTAAGTCACTCTGCTCTTGTGATCAGATGATCGAGCTGGGCCAAGATCTTAACATG 718
Qy 598 ACTTTAGCATGAAACTAATTAATGATCAAGATGAGCTTTTATTAACCTGATGCAAC 657
Db 719 ACGTTAAGCAAGGAAACTAAGGCTTAACCAAGATGAGCTTCTATTAACCTGATGAGCAAC 778
Qy 658 ATTGCTTTGACATCAATGAATCAATGAGAGAGCTTATGATGATGATGATGATGATG 717
Db 779 ATTTCCTTTGCGATCAATGAATCAATGAGAGAGCTTATGATGATGATGATGATGATG 838
Qy 718 GTTACGTCATGAATCAATGAATCAATGAGAGAGCTTATGATGATGATGATGATGATG 777
Db 839 GTTATGTCGTTAAACAGACATCAATGAGAGAGCTTATGATGATGATGATGATGATG 898
Qy 778 AGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837
Db 899 AGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 958
Qy 838 TTTTAAAGTACGCTGAGAGAGAAATGATGATGATGATGATGATGATGATGATGATGATG 897
Db 959 TTTTCAAGCTCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1018
Qy 898 GATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954
Db 1019 GATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1075

RESULT 6
US-08-842-842-6
; Sequence 6, Application US/08842842
; Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
```

REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 158..1105
US-08-842-842-6

Query Match 69.8%; Score 666.2; DB 2; Length 2295;
Best Local Similarity 82.5%; Pred. No. 1.5e-172;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 60
DB 158 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 217
QY 61 GGGCCCGGAGGCGCCGAGAGGCGCCCGCCAGCGCCGCGC---CGCGCGCTCGCGCGCAG 117
DB 218 GGGCCCGGAGGCGCCGAGAGGCGCCCGCCAGCGCCGCGC---CGCGCGCTCGCGCGCAG 277
QY 118 CAGCCCGCCGCGCCGCTCCGCTCATGTTCTGCGCCCTCTGGGGCTGGGGCTGGCGCAG 177
DB 278 CCGCCAGCCGCGCGCTCCGCTCATGTTCTGCGCCCTCTGGGGCTGGGGCTGGCGCAG 337
QY 178 GTTGTGTGAGAGGTGCGCCCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 237
DB 338 GTTGTGTGAGAGGTGCGCCCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 397
QY 238 TCAGAGATGAGCACTGCACTGATTTATAGATTTAGAGCTCCAGTAAATGAGATTT 297
DB 398 TCAGAGATGAGCACTGCACTGATTTATAGATTTAGAGCTCCAGTAAATGAGATTT 457
QY 298 CAGAGACAACTCTGAGAGTCAAGATACAAATTAATCTGATTTCAATGTAGAGAAAT 357
DB 458 CAGAGACAACTCTGAGAGTCAAGATACAAATTAATCTGATTTCAATGTAGAGAAAT 511
QY 358 AAGAGGCTTTTCAAGAGCTGAGCAAAAGGATTAACAATATCGTTGGATCAGCAGCAG 417
DB 512 AAGAGGCTTTTCAAGAGCTGAGCAAAAGGATTAACAATATCGTTGGATCAGCAGCAG 571
QY 418 ATCAGAGCAGAGAAAGCGATGTGTGATGGCTCATGTGATCTGAGCTGAGCAAGAGCAG 477
DB 572 TTCTCAGAGAGCTCAGCTATGATGAAAGGCTCATGTGATGTGAGCTGAGCAAGAGCAG 631
QY 478 CTGGAAGCTCAGCTTTTGTCTCATCTCATTAATGAGCCAGCATCCCATGCTGGTTC 537
DB 632 CCGAGAGGCGCCAGCTTTGAGCACTCAGCATTAATGAGCTGAGCAAGCTCCATGGGTTC 691
QY 538 CATTAAGTGTGCTGCTCTGTTGATACATGAGGAGTGGGCGCAAGATCTCCAAATG 597
DB 692 CATTAAGTGTGCTGCTCTGTTGATACATGAGGAGTGGGCGCAAGATCTCCAAATG 751
QY 598 ACTTTTGAAGTGAAGAACTAATAGTTAATCAGATGGCTTTTATTAATCTGATGCGCAC 657
DB 752 ACCTTGAAGTGAAGAACTAATAGTTAATCAGATGGCTTTTATTAATCTGATGCGCAC 811
QY 658 ATTGCTTTGACATCATGAACTTCAGGAGACTAGCTACAGAGTCTTCAAGTAAAG 717
DB 812 ATTGCTTTGACATCATGAACTTCAGGAGACTAGCTACAGAGTCTTCAAGTAAAG 871
QY 718 GTGAGTCACTAAAACCATATCAAAATCCAAAGTCTATACCCGATGAAAGAGGA 777
DB 872 GTGATATCTGTTAAACCATATCAAAATCCAAAGTCTATACCCGATGAAAGAGGA 931
QY 778 AGCAGCAAGATATGTTGAGGAAATCTGAATTCATTTTATTCATTAAGCTTTGTTGA 837
DB 932 AGCAGCAAGATATGTTGAGGAAATCTGAATTCATTTTATTCATTAAGCTTTGTTGA 991

QY 838 TTTTAAAGTACGCTGAGAGAGAAATCAAGATTCAGAGTCTCCACCCCTCTACTG 897
DB 992 TTTTAAAGTACGCTGAGAGAGAAATTCAGATTCAGAGTCTCCACCCCTCTACTG 1051
QY 898 GATCCGATCAGAGATGCAACATACCTTTGGGCTTTTAAAGTTCAGATATGATTGA 954
DB 1052 GATCCGATCAGAGATGCAACATACCTTTGGGCTTTTAAAGTTCAGATATGATTGA 1108

RESULT 7
US-09-052-521C-1
Sequence 1, Application US/09052521C
Patent No. 6316408
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451Bv
CURRENT FILING DATE: 1998-03-30
CURRENT APPLICATION NUMBER: US/09/052.521C
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2295
TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
LOCATION: (158)..(1105)
US-09-052-521C-1

Query Match 69.8%; Score 666.2; DB 4; Length 2295;
Best Local Similarity 82.5%; Pred. No. 1.5e-172;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 1 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 60
DB 158 ATGCGCCGCGCCAGAGAGACTACACCAAGTACCTGCTCGGAGAGATGGCGGC 217
QY 61 GGGCCCGGAGGCGCCGAGAGGCGCCCGCCAGCGCCGCGC---CGCGCGCTCGCGCGCAG 117
DB 218 GGGCCCGGAGGCGCCGAGAGGCGCCCGCCAGCGCCGCGC---CGCGCGCTCGCGCGCAG 277
QY 118 CAGCCCGCCGCGCCGCTCCGCTCATGTTCTGCGCCCTCTGGGGCTGGGGCTGGCGCAG 177
DB 278 CCGCCAGCCGCGCGCTCCGCTCATGTTCTGCGCCCTCTGGGGCTGGGGCTGGCGCAG 337
QY 178 GTTGTGTGAGAGGTGCGCCCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 237
DB 338 GTTGTGTGAGAGGTGCGCCCTGTTCTCTATTTCAGAGCGCAGATGATCTATAGATA 397
QY 238 TCAGAGATGAGCACTGCACTGATTTATAGATTTAGAGCTCCAGTAAATGAGATTT 297
DB 398 TCAGAGATGAGCACTGCACTGATTTATAGATTTAGAGCTCCAGTAAATGAGATTT 457
QY 298 CAGAGACAACTCTGAGAGTCAAGATACAAATTAATCTGATTTCAATGTAGAGAAAT 357
DB 458 CAGAGACAACTCTGAGAGTCAAGATACAAATTAATCTGATTTCAATGTAGAGAAAT 511
QY 358 AAGAGGCTTTTCAAGAGCTGAGCAAAAGGATTAACAATATCGTTGGATCAGCAGCAG 417
DB 512 AAGAGGCTTTTCAAGAGCTGAGCAAAAGGATTAACAATATCGTTGGATCAGCAGCAG 571
QY 418 ATCAGAGCAGAGAAAGCGATGTGTGATGGCTCATGTGATCTGAGCTGAGCAAGAGCAG 477
DB 572 TTCTCAGAGAGCTCAGCTATGATGAAAGGCTCATGTGATGTGAGCTGAGCAAGAGCAG 631
QY 478 CTGGAAGCTCAGCTTTTGTCTCATCTCATTAATGAGCCAGCATCCCATGCTGGTTC 537


```

0Y 782 CCAAGTATTGCTCAGGGGATTCGAATTCATTTTATTCGATPAAGGTGGGATTTT 84.1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 CGAANAACCTGGTCGGCCGCAATTCCTAATTCACCTTTTATTCATRAAATGTTGGGGATTTT 77.4
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 842 TTAAGTACGGCTCGAGAGAGAAATCAACATCGAGCTCCCAACCCCTCTACTGATC 90.1
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 TCAAGCTCCGAGCTGGTGTGAAGAAATTTAGCATTTAGGTGTCACACCCCTTCCTGCTGATC 83.4
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
0Y 902 CGGATCGAGATCGCAACATCTTTGGGGCTTTTAAAGTTCCAGATATATGATTTGA 95.4
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 835 CGGATCAAGATGCGACGCTACTTTGGGCGCTTTCAAAGTTCAAGACATAGACTGA 88.7
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-08-995-659-10
; Sequence 10, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Mariskovsky, Eugene
; TITLE OF INVENTION: Lysand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1630 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: RANKL
; FEATURE:

```

[illegible]


```

; SEQ ID NO 10
; LENGTH: 759
; TYPE: DNA
; ORGANISM: synthetic fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(759)
;
US-09-320-424-10

```

| | | | | |
|---------------------------|--------|------------------|-----------|------------|
| Query Match | 7.3%; | Score 69.4; | DB 4; | Length 75; |
| Best Local Similarity | 51.9%; | Pred. No. 1e-09; | | |
| Matches 182; Conservative | 0; | Mismatches 166; | Indels 3; | Gaps 1; |

| | | | |
|----|-----|--|-----|
| OY | 591 | CACATGACTTTTGGCAATGGAACAACTAATAGTTAAATCAGATGCGCTTTATATACCTGA | 650 |
| Db | 411 | caacttgaccttggaatgagtgacactgylcatccatgaaaaaggylttactacacta | 470 |
| OY | 651 | TGCCAACATTTTGCTTGGACATTCATGAAACTTCAGGAGACCTACTCTCAGAGTCTTCA | 710 |
| Db | 471 | ttcccaaacactcttcgactcatttcaggagaaataaaga---aaacaagaagcaca | 527 |
| OY | 711 | ACTATGGTGTCACGCTCCTAAACACAGATCAAAATCCCAAGTCTCATACCCGTATGAA | 770 |
| Db | 528 | acaaatggtcccaatatattacaataacaaagttatccctacatatgttgatgaa | 587 |
| OY | 771 | AGGAGAGACCAACGATATTGGTCAGGGAATTCGAATTCATTATTCATCAAAGT | 830 |
| Db | 588 | aagtgctgaaatagttgtgtctaaagatgacgaataatgactctatccatctatca | 647 |
| OY | 831 | TGGTGATTTTTTAAAGTTACGCTCTGGAGAGGAAATCAGCATCGAGGTCTCAACCCCTC | 890 |
| Db | 648 | agggggaatatttgagcttaagaaaatgacagaatttctgtctaaacaatgaca | 707 |
| OY | 891 | CTTACTGATCCGGATCAGAGATGCAAACTACTTGGGCTTTTAAAGTCG | 941 |
| Db | 708 | cttgtaagacatgagccatgaaagccagtttcttcggggccttctaagtttg | 758 |

RESULT 12
US-09-320-424-12
Sequence 12, Application US/09320424

GENERAL INFORMATION:

APPLICANT: Wilely, Steven R.
APPLICANT: Goodwin, Raymond G.

```

; TITLE OF INVENTION: Cytokine that Induces
; FILE REFERENCE: 2835-E

```

;; CURRENT APPLICATION NUMBER: US/09/320,424
;; CURRENT FILING DATE: 1999-05-26

```

; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10

```

EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26

EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25

; EARLIER APPLICATION NUMBER: 08/548,366
; EARLIER FILING DATE: 1995-11-01

; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29

```
; NUMBER OF SEQ ID NOS: 25
;
; SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 12
; LENGTH: 768

```

; TYPE: DNA
; ORGANISM: synthetic fusion
;

```

```
; FEATURE:
; NAME/KEY: CDS
```

LOCATION: (1
US-09-320-424-12

Query Match 7.3%; Score 69.4; DB 4; Length 768;

Best Local Similarity 51.9%; pred. No. 1.1e-09;
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 1

[illegible]

RESULT 13
US-08-584-031-2

; Sequence 2, Application
; Patent No. 6030945

```

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
;

```

;; TITLE OF INVENTION: APO-Z LIGAND
; FILE REFERENCE: 11669.22US03

```

; CURRENT APPLICATION NUMBER: 05/08/584,051A
; CURRENT FILING DATE: 1996-01-09

```

```

; NUMBER OF SEQ ID NOS: 1/
; SOFTWARE: PatentIn Ver. 2.0.0

```

; SEQ ID NO 2
; LENGTH: 1042
;

```

; TYPE: DNA
; ORGANISM: Homo sapiens

```

US-08-584-031-2

| Query Match | Score | DB | Length |
|-------------|-------|-------|--------|
| 7.3% | 69.4 | 3 | 1042 |
| 51.0% | 1 | 2e-09 | |

Best Local Similarity 51.58; Freq. NO. 4.26 0.7
Matches 182; Conservative 0; Mismatches 166; Indels 3; Gaps 17

591 CAACATGACTTTAGCAATGCAAACTAATAGTTAATCAGATGGCTTTTATTAACCTGTA 650

Db 585 caacttgcacttgaggaatgtgtgaactgtgtcattccatgaaaagggtttlactacatcta 644

651 TGGCAACATTTGCTTTGCACATCATGAACCTCAGGAGACCTAGCTTACAGAGTATCTTCA 710

Db 645 ttcccaaacatacttgcgatttcagaggaataaaga--aaacacaagaacgacaa 701

711 ACTAATGGTGTACGTCACATAAAACGACATCAAAATCCCAAGTTCATATACCTGATGAA 770
OY

Db 702 acaaatggtccaatatatttacaatacacagaattatcctgacctatatgttgatgaa 761

771 AGGAGGAGCACCAGTATTGTCAGGGAATTCTGAATTCATTTTTATTCATTAACGT 830

Db 762 aagtgctagaataatgttgtgctaaagatgcagaatatgtgactctattccatcatca 82

831 TGGTGCATTTTAAAGTTACGGTCTGAGAGGAATCAGCATGAGGCTCTCCAAACCCCTC 899

Db 822 agggggaatatatttgagcttaagaaatgacagaattttctgttaacaalpyagca 881

891 CTTACTGATCCGATCAGATCAACATCTTTGGGCTTTAAAGCTTCG 941

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 20:05:54 ; Search time 89.9 seconds
(without alignments)
391.662 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685
Sequence: 1 MRRASRDYRKYLGRSEEMG.....LDDPDADATYFGAFKVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SID55/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID55/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID55/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID55/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID55/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID55/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID55/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID55/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID55/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID55/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID55/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID55/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID55/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID55/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID55/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID55/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID55/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID55/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID55/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID55/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID55/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1685 | 100.0 | 317 | AAW83195 | Human osteoprotege |
| 2 | 1685 | 100.0 | 317 | AAW69957 | NE-KB receptor act |
| 3 | 1685 | 100.0 | 317 | AAW68293 | NE-KB receptor act |
| 4 | 1685 | 100.0 | 317 | AAW84417 | Amino acid sequenc |
| 5 | 1685 | 100.0 | 317 | AAW8738 | Human receptor act |
| 6 | 1685 | 100.0 | 317 | AAW04426 | Human receptor act |
| 7 | 1685 | 100.0 | 317 | AAW01993 | Human full-length |
| 8 | 1677 | 99.5 | 317 | AAW83018 | Osteoclastogenesis |
| 9 | 1417.5 | 84.1 | 316 | AAW83194 | Human osteoprotege |
| 10 | 1417.5 | 84.1 | 316 | AAW83017 | Osteoclastogenesis |
| 11 | 1417.5 | 84.1 | 316 | AAW59654 | Amino acid sequenc |

| | | | | | |
|----|--------|------|-----|----------|--------------------|
| 12 | 1417.5 | 84.1 | 316 | AAW17874 | Murine TRANCE. Mu |
| 13 | 1417.5 | 84.1 | 316 | AAW91024 | Mouse OBM protein |
| 14 | 1417.5 | 84.1 | 316 | AAW84418 | Amino acid sequenc |
| 15 | 1417.5 | 84.1 | 316 | AAW84419 | Amino acid sequenc |
| 16 | 1396.5 | 82.9 | 318 | AAW82092 | NF-KB receptor act |
| 17 | 1326.5 | 78.7 | 294 | AAW69956 | NF-KB receptor act |
| 18 | 1326.5 | 78.7 | 294 | AAW68292 | NF-KB receptor act |
| 19 | 1326.5 | 78.7 | 294 | AAW68737 | Murine receptor ac |
| 20 | 1326.5 | 78.7 | 294 | AAW04425 | Murine receptor ac |
| 21 | 1326.5 | 78.7 | 294 | AAW01992 | Murine RANKL (recc |
| 22 | 1294 | 76.8 | 246 | AAW83020 | Osteoclastogenesis |
| 23 | 1293 | 76.7 | 245 | AAW17873 | Human TRANCE. Hom |
| 24 | 1136 | 67.4 | 501 | AAW84420 | Amino acid sequenc |
| 25 | 1109 | 65.8 | 244 | AAW83019 | A murine OCIF-bind |
| 26 | 852 | 50.6 | 160 | AAW80273 | Amino acid sequenc |
| 27 | 814 | 48.3 | 152 | AAW67248 | Human RANKL. Homo |
| 28 | 790 | 46.9 | 170 | AAW08386 | Mouse FLAG-murine |
| 29 | 771 | 45.8 | 187 | AAW84420 | Amino acid sequenc |
| 30 | 769 | 45.6 | 173 | AAW84421 | Amino acid sequenc |
| 31 | 768 | 45.6 | 160 | AAW80272 | Amino acid sequenc |
| 32 | 759 | 45.0 | 173 | AAW84422 | A murine osteoprot |
| 33 | 721.5 | 42.8 | 188 | AAW84423 | An osteoprotegerin |
| 34 | 711.5 | 42.2 | 182 | AAW84424 | An osteoprotegerin |
| 35 | 691 | 41.0 | 173 | AAW84425 | DNA encoding osteo |
| 36 | 683 | 40.5 | 139 | AAW91023 | Mouse OBM protein |
| 37 | 670 | 39.8 | 173 | AAW84426 | An osteoprotegerin |
| 38 | 317.5 | 18.8 | 74 | AAW91020 | Mouse OBM protein |
| 39 | 252.5 | 15.0 | 281 | AAW27016 | Human Apo-2 ligand |
| 40 | 252.5 | 15.0 | 281 | AAW27017 | Human Apo-2 ligand |
| 41 | 251.5 | 14.9 | 279 | AAW6332 | Human TLR2 (TRAIL) |
| 42 | 251.5 | 14.9 | 279 | AAW5032 | Tumour necrosis fa |
| 43 | 251.5 | 14.9 | 281 | AAW27134 | Human Apoptosis in |
| 44 | 251.5 | 14.9 | 281 | AAW19787 | Human Apoptosis in |
| 45 | 251.5 | 14.9 | 281 | AAW19777 | Novel cytokine Apo |

ALIGNMENTS

| | | |
|----------|---|-------------------------------------|
| AAW83195 | 1 | AAW83195 standard; Protein: 317 AA. |
| XX | XX | |
| AC | AAW83195: | |
| XX | XX | |
| DT | 11-FEB-1999 (first entry) | |
| XX | XX | |
| DE | Human osteoprotegerin binding protein from the pcDNA/huOPGp1.1insert. | |
| XX | XX | |
| KW | Human; osteoprotegerin binding protein; OPG binding protein; arthriti | |
| KW | osteoporosis; osteoclast maturation; bone disease; metastasis; OMR; | |
| KW | hypercalcaemia; osteoclast differentiation and activation receptor; | |
| KW | Paget's disease. | |
| XX | XX | |
| OS | Homo sapiens. | |
| XX | XX | |
| PN | MO9846751-AA1. | |
| XX | XX | |
| PD | 22-OCT-1998. | |
| XX | XX | |
| PE | 15-APR-1998; 98WO-US07584. | |
| XX | XX | |
| PR | 30-MAR-1998; 98US-0052521. | |
| PR | 16-APR-1997; 97US-0842842. | |
| PR | 23-JUN-1997; 97US-0880855. | |
| XX | XX | |
| PA | (AMGE-) AMGEN INC. | |
| XX | XX | |
| PI | Boyle WJ; | |
| XX | XX | |
| DR | WPI: 1998-594578/50. | |
| DR | N-PSDB; AAW70285. | |
| XX | XX | |

```
PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
PS Claim 19; Fig 4; 47bp; English.
XX
CC The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OPG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX
SQ Sequence 317 AA;
Query Match 100.0%; Score 1685; DB 19; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYTKYLRGSEEGGPGARHGPRLNAPPPAHOPPAARSFVALLGIGLOV 60
DB 1 mrrasrdytkylrgseemgpgpaphhegplnappbhqppaarsmtfvallgiglv 60
QY 61 VCSVALFFYFRQMPNRISEDTGTCIYRILRLHFNADFODTLRSOPTKLIPDSCRIRK 120
DB 61 vcsvalffyfraqmndpnrlsedgtchcyrlrlrlnhenaqdtllsqdtkllpsdcrirk 120
QY 121 QAFQAVOKELQIHVSGSHIRAEKAMVDGSWDLAKRSKLEQAPPAHLTINATDIPSGSH 180
DB 121 qafqavokelqihvsgshiraeakamvdgswldakrskleaqppahltinatdipsgsh 180
QY 181 KVSLSWYHNRGMWAKISNMTFNSNGKLIYNQGFYLYANICRHNHETSGDLATEYLQIMV 240
DB 181 kvslswwyhdrgwakismtfnsgkliyngdgylyanicttrhnetsgdlateylqimv 240
QY 241 VYTKSIRKIPSSHTLMKGGSTKYWGNSPEHFYSINVGGEFKLRGSEETISIEVSNPSILD 300
DB 241 yvtksirkipshtlmkgsstkyswgnspehfysinvvgffklrsgseelsievnpsild 300
QY 301 PDQDATYFGAFKVRDID 317
DB 301 pdqdatyfgafkvridd 317
RESULT 2
AAW69957
ID AAW69957 standard; Protein; 317 AA.
XX
AC AAW69957;
XX
DB 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL).
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
OS Homo sapiens.
XX
XX WO9828426-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
XX
XX 14-OCT-1997; 97US-0064671.
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0813509.
XX
XX (IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WPI: 1998-377657/32.
XX
XX N-PSDB; AAW41378.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
XX develop products for augmenting an immune response for inhibiting an
XX inflammatory response and for protection of cells
XX
XX Claim 27; Pages 59-60; 80pp; English.
XX
XX This represents a human RANKL, a ligand for the RANK (receptor
XX activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
XX member of the tumour necrosis factor (TNF) family. A soluble RANK
XX may be used for inhibiting activation of NF-kB, by contacting a cell
XX expressing membrane-associated RANK with a soluble RANK which binds to
XX RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
XX used to induce maturation of dendritic cells and enhance their
XX allo-stimulatory capacity, thereby augmenting an immune response. The
XX soluble RANK polypeptide composition may also be used for regulating an
XX immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
XX may be useful in ameliorating negative effects of an inflammatory
XX response that result from triggering of RANK, e.g. in treating toxic
XX shock or sepsis, graft-versus-host reactions, or acute inflammatory
XX reactions. They can also be used in adjunct therapy for disease
XX characterised by neoplastic cells that express RANK. RANKL polypeptides
XX can also be used to identify inhibitors of RANK and thus inhibitors of
XX an inflammatory response, and also for protecting RANK-expressing cells
XX from the negative effects of chemotherapy or the presence of high levels
XX of TNF-alpha. The products can also be used for detection and drug
XX screening.
XX
XX Sequence 317 AA;
Query Match 100.0%; Score 1685; DB 19; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYTKYLRGSEEGGPGARHGPRLNAPPPAHOPPAARSFVALLGIGLOV 60
DB 1 mrrasrdytkylrgseemgpgpaphhegplnappbhqppaarsmtfvallgiglv 60
QY 61 VCSVALFFYFRQMPNRISEDTGTCIYRILRLHFNADFODTLRSOPTKLIPDSCRIRK 120
DB 61 vcsvalffyfraqmndpnrlsedgtchcyrlrlrlnhenaqdtllsqdtkllpsdcrirk 120
QY 121 QAFQAVOKELQIHVSGSHIRAEKAMVDGSWDLAKRSKLEQAPPAHLTINATDIPSGSH 180
DB 121 qafqavokelqihvsgshiraeakamvdgswldakrskleaqppahltinatdipsgsh 180
QY 181 KVSLSWYHNRGMWAKISNMTFNSNGKLIYNQGFYLYANICRHNHETSGDLATEYLQIMV 240
DB 181 kvslswwyhdrgwakismtfnsgkliyngdgylyanicttrhnetsgdlateylqimv 240
QY 241 VYTKSIRKIPSSHTLMKGGSTKYWGNSPEHFYSINVGGEFKLRGSEETISIEVSNPSILD 300
DB 241 yvtksirkipshtlmkgsstkyswgnspehfysinvvgffklrsgseelsievnpsild 300
QY 301 PDQDATYFGAFKVRDID 317
```

```

Db      301  pdqdaelyfgafkvrld 317
      |||
RESULT  3
AAW68293
ID      AAW68293 standard; Protein: 317 AA.
AC      AAW68293;
XX
XX      08-OCT-1998 (first entry)
DT
DE      NF-kB receptor activator RANK ligand (RANKL).
XX
XX      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW      immune response; inflammatory response; toxic shock; sepsis;
KW      RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
OS      Homo sapiens.
XX
XX      MO9828424-A2.
PN
XX      02-JUL-1998.
PD
XX      22-DEC-1997; 97MO-US23866.
PF
XX      14-OCT-1997; 97US-0064671.
PR      23-DEC-1996; 96US-0059978.
PR      07-MAR-1997; 97US-0813509.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX      WPI: 1998-377655/32.
DR      N-PSDB: AAV41372.
XX
XX      New isolated receptor activator of necrosis factor-kappa B - useful
PT      for, e.g. developing products for regulating an immune or
PT      inflammatory response, treating toxic shock or sepsis
XX
XX      Example 7: Pages 59-60; 80pp; English.
XX
CC      This represents a human RANKL, a ligand for the RANK (receptor
CC      activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC      member of the tumour necrosis factor (TNF) family. Host cells transformed
CC      or transfected with an expression vector comprising the RANK encoding
CC      nucleic acid can be used to produce recombinant RANK protein. The soluble
CC      RANK may be used for inhibiting activation of NF-kB by contacting a cell
CC      expressing membrane-associated RANK with a soluble RANK which binds to
CC      RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC      used for regulating an immune or inflammatory response. Inhibition of
CC      NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC      of an inflammatory response that result from triggering of RANK, e.g. in
CC      treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC      inflammatory reactions. They can also be used in adjunct therapy for
CC      disease characterised by neoplastic cells that express RANK. The products
CC      can also be used for detection and drug screening.
XX
XX      Sequence 317 AA:
XX
Query Match      100.0%; Score 1685; DB 19; Length 317;
Best Local Similarity 100.0%; Pred. No. 2,6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      121  OAFQAVOKELQHTVGSQHIRAEKAWYDGSWLDIAKRSKLEAOPFAHLLTNATDIPSGSH 180
      |||
Db      121  qafgavqkqlghlvgsqhnraekamwgsvlidlakrskleaqpfahlllnatdipsgsh 180
OY      181  KVSLSWYHNRGMAKISNMFPSNCKLIYNODGFYYLAAVICFRHHETSGDLATEYDLMV 240
      |||
Db      181  kvslsswyhndrgwakismnctsnngkllvngdgfyylyanlcfrhetsksgdlateyldlmv 240
OY      241  YVTKTSIKIPSSHTLMKGSTKTVSGNSSEPHYSINVGFEFKLRSGEISIEVSNPSILD 300
      |||
Db      241  yvktkslkipsshclmkgstlkysgnssefhfysinvgffklrsgelsievsnpald 300
OY      301  PDODATYEGAFKVRDID 317
      |||
Db      301  pdqdaelyfgafkvrld 317

RESULT  4
AAV84417
ID      AAV84417 standard; Protein: 317 AA.
XX
XX      AAV84417;
AC
XX      25-JUL-2000 (first entry)
DT
XX      Amino acid sequence of a human osteoprotegerin ligand (OPGL).
DE
XX
XX      Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW      tumour necrosis factor receptor; type II transmembrane protein;
KW      osteoclast differentiation; CSF-1; osteoclast activator;
KW      immune response; osteoporosis; bone resorption.
XX
XX      Homo sapiens.
OS
XX
XX      Key
XX      Region
XX      Location/Qualifiers
XX      49..69
XX      /note="Transmembrane region"
XX      70..157
XX      /note="extracellular stalk domain"
XX      158..317
XX      /note="active ligand moiety"
XX
XX      WO200015807-A1.
XX
XX      23-MAR-2000.
PD
XX      13-SEP-1999; 99MO-DK00481.
PF
XX      15-SEP-1998; 98DK-0001164.
PR      02-OCT-1998; 98US-0102896.
XX
XX      (MEB-) M & E BIOTECH AS.
XX
XX      Halkier T, Haanling J;
XX
XX      WPI: 2000-271444/23.
DR      N-PSDB: AAV99964.
XX
XX      In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT      to treat, prevent and ameliorate osteoporosis -
XX
XX      Claim 19: Page 78-79; 110pp; English.
XX
CC      The present sequence represents a human osteoprotegerin ligand (OPGL).
CC      Osteoprotegerin is a secreted member of the tumour necrosis factor
CC      receptor family, which blocks osteoclastogenesis in a dose dependent
CC      manner. The OPGL protein is synthesised as a type II transmembrane
CC      protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC      is a potent osteoclast differentiation factor when combined with CSF-1.
CC      It is not capable of inducing osteoclast differentiation in the absence
CC      of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC      specification describes a method for the in vivo down-regulation of

```

CC OPGl activity in an animal. The method comprises using at least one OPGl
 CC polypeptide or subsequence, and/or at least one OPGl analogue to induce
 CC an immune response in the animal. The method and OPGl polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 317 AA:

Query Match 100.0%; Score 1685; DB 21; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2,6e-156;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSGEMGGPGAPHECPHLAPPPAPHPAPASRSMFVALLGLGIGOV 60
 DB 1 mrrasrdytkylrgseemggpgaphegplhappppahqppaasrsmfval191919qv 60
 QY 61 VCSVALFFYFRAQMDPNRISDGTGHCYRILRLHENDFQDTTLESODTKLIPDSCRRIK 120
 DB 61 vcsvalffyfraqmdpnrisedgtchcylrlrlhenedfgdtlesqdklpsccrik 120
 QY 121 QAFQAVOKELQHTVSGOHIRAEKAMVDGSMWLAKNSKLEAPPAHLTNATDIPSGSH 180
 DB 121 qafgavokelqhtvsgohiraekamvdgswldakrskleapfahltnatdipsqsh 180
 QY 181 KVSLSWYHDSGMAKISMTFSNGKLIYNODGFYLVANICFRHNETSGDLATEYLQAMV 240
 DB 181 kvsisswyhdsywakismfnsngklyvngdgylyanlcfrihnetsgdaleylqamv 240
 QY 241 YVTKTSIKIPSSHTLMKGSTKRYWNGSEFHFYSINVGPFKRLSGEISIEVSNPSILD 300
 DB 241 yvktstikipshtlmkgsstkrywngsefhfysinvgpfkrlsgesievsnpssild 300
 QY 301 PDQATYFGAFKVRDID 317
 DB 301 pdqatfygafkvridd 317

RESULT 5
 AAE08738
 ID AAE08738 standard; Protein: 317 AA.
 XX
 AC AAE08738;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Human receptor activator of NF kappaB ligand (RANKL) protein.
 XX
 KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 PN US6271349-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 17-DEC-1998; 98US-0215649.
 XX
 PR 23-DEC-1996; 96US-0059978.
 PR 14-MAR-1997; 97US-0071181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Dougal WC, Galibert L;

DR WPI: 2001-520313/57.
 DR N-PSDB: AAD15311.

PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK

XX Example 15; Column 71-72; 47pp; English.

CC The patent discloses novel receptor activator of nuclear factor (NF)-
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
 CC of the tumour necrosis factor (TNF) receptor superfamily and associates
 CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
 CC in the regulation of immune and inflammatory response. The receptors
 CC are useful for regulating immune response and in screening for inhibitors
 CC of these receptors. The cytoplasmic domain of RANK is used in developing
 CC assays for inhibitors of signal transduction, e.g. for screening the
 CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
 CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
 CC are useful in ameliorating the negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, acute inflammatory
 CC reactions and the effects of bone resorption. RANK acts as an anti-
 CC apoptotic signal and rescue the cells that express RANK from apoptosis.
 CC Soluble forms of the receptor are used in vivo or in vitro based
 CC screening tests for agonists or antagonists of RANK activity, as
 CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
 CC transduction of a signal via RANK. RANK compositions are used in the
 CC development of both agonistic and antagonistic antibodies, or as an
 CC adjunct therapy for disease characterised by neoplastic cells that
 CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
 CC are useful for modulating the formation of osteoclasts from osteoclast
 CC precursors and for modulating osteoclast function and activities. They
 CC are used as inhibitors of diseases associated with excess bone resorption
 CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
 CC useful for the expression of recombinant proteins, as probes for analysis
 CC of the presence or distribution of RANK transcripts, while the proteins
 CC are useful in preparing kits for the detection of soluble RANK, or
 CC monitor RANK-related activity. The present sequence is RANK ligand
 CC (RANKL) protein from human.

XX Sequence 317 AA:

Query Match 100.0%; Score 1685; DB 22; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2,6e-156;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSGEMGGPGAPHECPHLAPPPAPHPAPASRSMFVALLGLGIGOV 60
 DB 1 mrrasrdytkylrgseemggpgaphegplhappppahqppaasrsmfval191919qv 60
 QY 61 VCSVALFFYFRAQMDPNRISDGTGHCYRILRLHENDFQDTTLESODTKLIPDSCRRIK 120
 DB 61 vcsvalffyfraqmdpnrisedgtchcylrlrlhenedfgdtlesqdklpsccrik 120
 QY 121 QAFQAVOKELQHTVSGOHIRAEKAMVDGSMWLAKNSKLEAPPAHLTNATDIPSGSH 180
 DB 121 qafgavokelqhtvsgohiraekamvdgswldakrskleapfahltnatdipsqsh 180
 QY 181 KVSLSWYHDSGMAKISMTFSNGKLIYNODGFYLVANICFRHNETSGDLATEYLQAMV 240
 DB 181 kvsisswyhdsywakismfnsngklyvngdgylyanlcfrihnetsgdaleylqamv 240
 QY 241 YVTKTSIKIPSSHTLMKGSTKRYWNGSEFHFYSINVGPFKRLSGEISIEVSNPSILD 300
 DB 241 yvktstikipshtlmkgsstkrywngsefhfysinvgpfkrlsgesievsnpssild 300
 QY 301 PDQATYFGAFKVRDID 317
 DB 301 pdqatfygafkvridd 317

```
RESULT 6
AAE04426
ID AAE04426 standard; Protein: 317 AA.
XX
AC AAE04426;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human receptor activator of NF-chl B ligand (huRANKL) protein.
XX
KW Human: receptor activator of NF-chl B; RANK; tumour necrosis factor; TNF;
KW CD40; TNF receptor-associated factor; TRAF; ligand; Immune response;
KW Chromosome 10q22.1; huRANKL; chromosome 13q14; transmembrane protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 162..317
ET /note="Receptor binding region"
XX
PN US6242213-B1.
XX
PD 05-JUN-2001.
XX
PE 22-DEC-1997; 97US-0995659.
XX
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
XX
PA (IMMUNEX CORP.
XX
PI Anderson DM;
XX
DR WPI: 2001-407216/43.
DR N-PSDB; AAD08715.
XX
PT New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF-chl B
PT receptor activator) of the receptor activator of NF-chl B (RANK)
XX
PS Claim 1; Column 65-66; 43pp; English.
XX
CC The present invention relates to receptor activator of NF-chl B (RANK)
CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular
CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
CC The ligands are useful for regulating immune response and in screening
CC for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
CC protein.
CC
SQ Sequence 317 AA;
XX
XX
Query Match 100.0%; Score 1685; DB 22; Length 317;
Best Local Similarity 100.0%; Pred. No. 2, 6e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 181 KVSLSWYHDSGRMAKISNMFPSNGKLIYNODGFYLYANICFRHHETSGDLATEYLQMV 240
|
Db 181 kvsisswyhdgrwakiisnmltsngkllvngdgylyianicfrhsetsgdlatey1q1mv 240
QY 241 YVTKTSIKIPSSHTLMKGSTKRYWGSNSEFHFYSINVGCFKLRSGEISIEVSNPGLD 300
|
Db 241 yvktstiklpsshclmkgstlkywsngsefhfyslnvggffklrsgeisievsnplld 300
QY 301 PDDATYFGAKRYVDID 317
|
Db 301 pdgdatyfgalkryvdid 317
XX
RESULT 7
AAE01993
ID AAE01993 standard; Protein: 317 AA.
XX
AC AAE01993;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human full-length RANKL (receptor activator of NF-kappab ligand).
XX
KW Human; receptor activator of NF-kappab; RANK; nuclear factor-kappab;
KW NF-kappab; tumour necrosis factor; TNF; type I transmembrane protein;
KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetrotic;
KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
KW immune system dysfunction; familial expansile osteolysis; FEO;
KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
XX
OS Homo sapiens.
XX
PN WO200136637-A1.
XX
PD 25-MAY-2001;
XX
PE 14-NOV-2000; 2000WO-US31459.
XX
PR 17-NOV-1999; 99US-0442029.
XX
PA (IMMUNEX CORP.
XX
PI Anderson DM, Hughes AE;
XX
DR WPI: 2001-329222/34.
DR N-PSDB; AAD05904.
XX
PT New DNA encoding a receptor activator of NF-kappab polypeptide for the
PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX
PS Disclosure: Page 76-77; 96pp; English.
XX
CC The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)-kappab), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a type I
CC transmembrane protein that interacts with TNF receptor-associated
CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
CC of the transcription factor NF-kappab, a ubiquitous transcription factor
CC that is most extensively utilised in cells of the immune system.
CC Inhibition of NF-kappab by RANK antagonists is useful in ameliorating
CC negative effects of inflammatory reactions, and the effects of excess
CC bone resorption. The RANK DNAs, proteins and their analogues are useful
CC for the preparation of pharmaceutical compositions, for infecting target
CC cells for use in gene therapy applications in diagnosing diseases
CC associated with RANK, and as targets for use in screening assays. They
CC may be used in the treatment or diagnosis of immune system dysfunction.
CC The present invention also encompasses gene therapy methods to correct
CC gene-activating mutations, associated with e.g. familial expansile
CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present amino acid sequence is full-length human RANKL (huRANKL)
CC protein. The RANKL gene is located in chromosome 13q14.
```

XX SQ Sequence 317 AA;
 Query Match 100.0%; Score 1685; DB 22; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSSEMGSGPAPHEGPHLAPPAPHPAPPAASRSMFYALLGLGLGV 60
 Db 1 mrrasrdytkylrsgseemggsgpapherplhappppahqpaasrsmfvallglglyqv 60
 QY 61 VCSVALFFPFRQMDPNRISDGHCIYRILRLHENDFODTTLESODTKLIPSCRRIK 120
 Db 61 vcsvalffpfrqmdpnrisedghciyrilrlhena dfgdtlesqdklipscrrik 120
 QY 121 QAFQAVQKELOHTVGSOHTRAEKAMVDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 180
 Db 121 qafgavqkelqhtvsgshtraekamvdgswldlaksrskleagpfahltinatdipsgsh 180
 QY 181 KVSLSWTHDRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQLMV 240
 Db 181 kvsllswthdrgmakismnmtfsgnkliynodgfylylanicfrhhetsgdlateylqlmv 240
 QY 241 YVTKTSIKIPSSHTLMKGSRTKWSGSEFHFYSINNGFPKLSGEISTEVSNPSTLD 300
 Db 241 yvtktsikipshtlmkgsrtkwsngsefhfysinvgffklsgeistevsnpstld 300
 QY 301 PDODATYFGAFKVRDID 317
 Db 301 pdodatyfga fkvrdid 317

RESULT 8
 AAM83018
 ID AAM83018 standard; Protein: 317 AA.
 XX AC AAM83018;
 XX DT 10-FEB-1999 (first entry)
 XX DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human.
 XX OS Homo sapiens.
 XX PN W09846644-A1.
 XX PD 22-OCT-1998.
 XX PF 15-APR-1998; 98WO-JP01728.
 XX PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 DR WPI: 1998-594563/50.
 DR N-PSDB: AAV69887.
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism

XX PS Claim 36; Pages 113-114; 151pp; Japanese.
 XX CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 XX SQ Sequence 317 AA;
 Query Match 99.5%; Score 1677; DB 19; Length 317;
 Best Local Similarity 99.7%; Pred. No. 1.6e-155;
 Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSSEMGSGPAPHEGPHLAPPAPHPAPPAASRSMFYALLGLGLGV 60
 Db 1 mrrasrdytkylrsgseemggsgpapherplhappppahqpaasrsmfvallglglyqv 60
 QY 61 VCSVALFFPFRQMDPNRISDGHCIYRILRLHENDFODTTLESODTKLIPSCRRIK 120
 Db 61 vcsvalffpfrqmdpnrisedghciyrilrlhena dfgdtlesqdklipscrrik 120
 QY 121 QAFQAVQKELOHTVGSOHTRAEKAMVDGSWLDLAKRSKLEAOPFAHLTINATDIPSGSH 180
 Db 121 qafgavqkelqhtvsgshtraekamvdgswldlaksrskleagpfahltinatdipsgsh 180
 QY 181 KVSLSWTHDRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQLMV 240
 Db 181 kvsllswthdrgmakismnmtfsgnkliynodgfylylanicfrhhetsgdlateylqlmv 240
 QY 241 YVTKTSIKIPSSHTLMKGSRTKWSGSEFHFYSINNGFPKLSGEISTEVSNPSTLD 300
 Db 241 yvtktsikipshtlmkgsrtkwsngsefhfysinvgffklsgeistevsnpstld 300
 QY 301 PDODATYFGAFKVRDID 317
 Db 301 pdodatyfga fkvrdid 317

RESULT 9
 AAM83194
 ID AAM83194 standard; Protein: 316 AA.
 XX AC AAM83194;
 XX DT 11-FEB-1999 (first entry)
 XX DE Human osteoprotegerin binding protein from the 32D-F3 ins.
 XX KW Human; osteoprotegerin binding protein; OPB binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODR;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease.
 XX OS Homo sapiens.
 XX PN W09846751-A1.
 XX PD 22-OCT-1998.
 XX PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 PA (AMGE-) AMGEN INC.
 PI Boyle WJ.
 DR WPI: 1998-594578/50.
 DR N-PSDB; AAV70284.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 PS
 PS Claim 19; Fig 1; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 CC
 XX
 XX Sequence 316 AA:
 SQ
 Query Match 84.1%; Score 1417.5; DB 19; Length 316;
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

AC AAM83017;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX
 XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KM osteoclast; bone absorption factor; bone disorder; calcium metabolism.
 XX
 OS Unidentified.
 XX
 PN WO9846644-A1.
 XX
 XX 22-OCT-1998.
 PD
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 XX WPI: 1998-594563/50.
 DR N-PSDB; AAV69886.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 PS
 PS Claim 8; Pages 106-108; 151pp; Japanese.
 XX
 CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilization of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilized form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 CC
 XX
 XX Sequence 316 AA:
 SQ
 Query Match 84.1%; Score 1417.5; DB 19; Length 316;
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;


```

Db 61 vvcsialfifraqmdpnrlsedschcfyrlrlhenagldstlesedc--lpdscrm 118
OY 120 KOAFQGAVOKELOHIYVGSQHTRAEKAWVDGSMDLAKRSKLEAOPFAHLTINATDIPSGS 179
Db 119 kqafgavqkelqnlvppqrfsgapammegswldvaq:qkpeaqpfahltinaasips 178
OY 180 HKVSLSSWYHDSGNAKISNMTFSNGKLIYNODGEFYLYANICFRHHETSGLATEYLQIM 239
Db 179 hkvltswyhdrgwaksnmclnsngkltrngdgfylyanlcfthetsgsvptdyqlm 238
OY 240 VYVTKTSIKIPSSHTLAKGSGSTKTYWGSNEFHFYSINVGFFKLRSGEISIEVSNPSLL 299
Db 239 vyvvtksiklpsshlmkgscknwsnsefthfysinvgffklragselisyvsnpsll 298
OY 300 DPDDATYEGAFKVRDID 317
Db 299 dpdgdalyfgafkvqdl 316

```

Search completed: July 8, 2002, 20:05:55
 Job time: 699 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: July 8, 2002, 20:01:06 ; Search time 52.39 Seconds
(without alignments)
147.794 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685

Sequence: 1 MRRASRDYTKYLGRSEMG.....LDDPDQATYFGAFKVRDID 317

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCMTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1685 | 100.0 | 317 | 3 | US-08-996-139-13 |
| 2 | 1685 | 100.0 | 317 | 4 | US-08-995-659-13 |
| 3 | 1685 | 100.0 | 317 | 4 | US-09-215-649A-13 |
| 4 | 1685 | 100.0 | 317 | 4 | US-09-052-521C-4 |
| 5 | 1417.5 | 84.1 | 316 | 2 | US-08-842-842-7 |
| 6 | 1417.5 | 84.1 | 316 | 4 | US-08-989-362-2 |
| 7 | 1417.5 | 84.1 | 316 | 4 | US-09-052-521C-2 |
| 8 | 1336.5 | 78.7 | 294 | 3 | US-08-996-139-11 |
| 9 | 1336.5 | 78.7 | 294 | 4 | US-08-995-659-11 |
| 10 | 1336.5 | 78.7 | 294 | 4 | US-09-215-649A-11 |
| 11 | 1251.5 | 14.9 | 279 | 4 | US-09-072-933C-3 |
| 12 | 1251.5 | 14.9 | 281 | 1 | US-08-670-354-2 |
| 13 | 1251.5 | 14.9 | 281 | 3 | US-08-584-031-1 |
| 14 | 1251.5 | 14.9 | 281 | 3 | US-08-780-496-1 |
| 15 | 1251.5 | 14.9 | 281 | 4 | US-08-883-086-10 |
| 16 | 1251.5 | 14.9 | 281 | 4 | US-09-320-424-2 |
| 17 | 1251.5 | 14.9 | 281 | 4 | US-09-333-593A-6 |
| 18 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 19 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 20 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 21 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 22 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 23 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 24 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 25 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 26 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |
| 27 | 1251.5 | 14.9 | 281 | 1 | US-09-320-424-6 |

| | | | | | | |
|----|-------|------|-----|---|------------------|--------------------|
| 28 | 189 | 11.2 | 281 | 4 | US-09-290-640-25 | Sequence 25, Appl |
| 29 | 189 | 11.2 | 281 | 4 | US-09-479-524-3 | Sequence 3, Appl1 |
| 30 | 189 | 11.2 | 281 | 4 | US-08-339-214-8 | Sequence 8, Appl1 |
| 31 | 189 | 11.2 | 281 | 4 | US-08-339-214-30 | Sequence 2, Appl1 |
| 32 | 189 | 11.2 | 281 | 5 | PCT-US95-00362-2 | Sequence 2, Appl1 |
| 33 | 184.5 | 10.9 | 279 | 4 | US-08-339-214-24 | Sequence 24, Appl |
| 34 | 184.5 | 10.9 | 279 | 5 | US-08-339-214-32 | Sequence 32, Appl |
| 35 | 184.5 | 10.9 | 279 | 5 | PCT-US95-00362-5 | Sequence 5, Appl1 |
| 36 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-16 | Sequence 16, Appl |
| 37 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-26 | Sequence 26, Appl1 |
| 38 | 164.5 | 9.8 | 376 | 3 | US-08-751-512-8 | Sequence 8, Appl1 |
| 39 | 158.5 | 9.4 | 261 | 1 | US-07-940-605A-2 | Sequence 2, Appl1 |
| 40 | 158.5 | 9.4 | 261 | 1 | US-08-184-422-8 | Sequence 8, Appl1 |
| 41 | 158.5 | 9.4 | 261 | 1 | US-08-360-823A-2 | Sequence 2, Appl1 |
| 42 | 158.5 | 9.4 | 261 | 1 | US-08-446-822-4 | Sequence 4, Appl1 |
| 43 | 158.5 | 9.4 | 261 | 2 | US-08-431-055-4 | Sequence 4, Appl1 |
| 44 | 158.5 | 9.4 | 261 | 2 | US-08-690-096-2 | Sequence 2, Appl1 |
| 45 | 158.5 | 9.4 | 261 | 2 | US-08-249-189-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-996-139-13
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13

| | | | |
|----|-----|---|-----|
| QY | 120 | KOAFQAGVOKELHITVSSONHRAKKAWDSSDILARSKYLEOPFHLITNTDIPSGS | 179 |
| | 119 | KOAFQAGVOKELHITVORQFSGSRRAMBSWYLDVORGRPEORANHLITNASSIPSGS | 178 |
| QY | 180 | HKVSLSMWYHDRCMAKISNMTFNSGKLLIVNODGFYUUYANICRRNHETSGDLATEYLOIM | 239 |
| | 179 | HKVTLSSWYHDRCMAKISNMTLSNGKLRVNOODGFYUUYANICRRNHETSGSVPEYLOIM | 238 |
| QY | 240 | VYVYKTSIKIPSSHTLMMKGGSTKWSNSNPFHFSINVGGRFKLRSEELISVNSPDL | 239 |
| | 239 | VYVYKTSIKIPSSHNLMKGGSTKWSNSNPFHFSINVGGRFKLRAGEELISVNSPDL | 238 |
| QY | 300 | DPDODATYFGAFKVRJID 317 | |
| | 299 | DPDODATYFGAFKYODID 316 | |

RESULT 6
US-08-989-362-2
; Sequence 2, Application US/08989362

GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-989-362-2

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 84.1%; | Score 1417.5; | DB 4; | Length 316; |
| Best Local Similarity | 84.3%; | Pred. No. 1.9e-136; | | |
| Matches 268; | Conservative 16; | Mismatches 31; | Indels 3; | Gaps 2. |

| | | | |
|----|----|--|-----|
| QY | 1 | MRRASRDTYTKLRGSEEMGGGPGAPNHEBPLH - APPRAPHQPPAASMSMVALLGLGLGQ | 59 |
| Db | 1 | MRRASRDYDGLTKLRSEEMGGGPGVPHBEPPLHAPASAPAPAPPAASMSMVALLGLGLGQ | 60 |
| QY | 60 | WVCSYALFFPYRPAQMDPNRISIEDGTHCYIRLLRLHENAPODTTLLESQDTKLIPDSCR I | 119 |
| Db | 61 | WVCSYALFLPYRPAQMDPNRISIEDSTHCCYIRLLRLHENAQDSTLLESDT - LPDSCRIM | 118 |

[illegible]

RESULT 7
US-09-052-521C-2
; Sequence 2, Application US/09052521C

```

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451B1V
CURRENT APPLICATION NUMBER: US/09/052,521C
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: Mouse
OS-09-052-521C-2

```

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 84.1%; | Score 1417.5; | DB 4; | Length 316; |
| Best Local Similarity | -84.3%; | Pred. No. 1.9e-136; | | |
| Matches 268; | Conservative 16; | Mismatches 31; | Indels 3; | Gaps 2; |

[illegible]

RESULT 8
US-08-996-139-11
; Sequence 11, Application US/08996139


```
Patent No. 6017729
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,139
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-996-139-11
```

```
Query Match 78.7%; Score 1326.5; DB 3; Length 294;
Best Local Similarity 84.5%; Pred. No. 3.2e-127;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 23 GAPHEGPLH-APPAPHPAPPAASRSMFVALLGLGLOVNCVSLFFFRQMDPNRISE 81
D 1 GVPHGSLHPPAPAPAPAPPAASRSMFVALLGLGLOVNCVSLFFFRQMDPNRISE 60
QY 82 DGTICIRILRLHFNADFDOTLTLESQDTKLIPDSGRIRKQAFQAVQKELQHYGSOHIR 141
D 61 DSTHCFYRILRLHFNADFDOTLTLESQDTKLIPDSGRIRKQAFQAVQKELQHYGSOHIR 118
QY 142 AEKAMVDSWMLDLAKRKLAPRAHLLTNATDIPSGSHKVSLSWYHNRGMKISNMTF 201
D 119 GAPAMMGSLDVAQKRPAPRAHLLTNATDIPSGSHKVSLSWYHNRGMKISNMTL 178
QY 202 SNGKLIYNQDGFYLLYANICFRHNETSGDLATEYLQLMVYVTKTSIKIPSSHLMKGGST 261
D 179 SNGKLIYNQDGFYLLYANICFRHNETSGSVPTDYLQLMVYVTKTSIKIPSSHLMKGGST 238
QY 262 KYNSGNSFHHYTSINNGCFKLSGGEISTEVSNPSLDPPQDATYTGAFVNRID 317
D 239 KNSGNSFHHYTSINNGCFKLSGGEISTEVSNPSLDPPQDATYTGAFVNRID 294
```

```
RESULT 9
US-08-995-659-11
: Sequence 11, Application US/08995659
: Patient No. 6242213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-995-659-11
```

```
Query Match 78.7%; Score 1326.5; DB 4; Length 294;
Best Local Similarity 84.5%; Pred. No. 3.2e-127;
Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;

QY 23 GAPHEGPLH-APPAPHPAPPAASRSMFVALLGLGLOVNCVSLFFFRQMDPNRISE 81
D 1 GVPHGSLHPPAPAPAPAPPAASRSMFVALLGLGLOVNCVSLFFFRQMDPNRISE 60
QY 82 DGTICIRILRLHFNADFDOTLTLESQDTKLIPDSGRIRKQAFQAVQKELQHYGSOHIR 141
D 61 DSTHCFYRILRLHFNADFDOTLTLESQDTKLIPDSGRIRKQAFQAVQKELQHYGSOHIR 118
QY 142 AEKAMVDSWMLDLAKRKLAPRAHLLTNATDIPSGSHKVSLSWYHNRGMKISNMTF 201
D 119 GAPAMMGSLDVAQKRPAPRAHLLTNATDIPSGSHKVSLSWYHNRGMKISNMTL 178
QY 202 SNGKLIYNQDGFYLLYANICFRHNETSGDLATEYLQLMVYVTKTSIKIPSSHLMKGGST 261
D 179 SNGKLIYNQDGFYLLYANICFRHNETSGSVPTDYLQLMVYVTKTSIKIPSSHLMKGGST 238
```



```
STATE: MA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670.354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496.632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548.368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

Query Match      14.9%  Score 251.5; DB 1; Length 281;
Best Local Similarity 24.1%  Pred. No. 1.4e-17;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY  42 PAASRMEFALLGLGQVCSVALFEFFRAQMD--PRISEDGTHCIYRLRLHENDF 99
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  10 PSLGQTCVLIYFVYLLQSLCAVATYYFTNELKQMDKYSKSIACE-----LKED--- 61
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  100 QDTILESODTKLIPDSRRITQAFQAVQKELQHIYVGSQHTRAEKAVYDGSMDLAKRSK 159
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  62 -DSYWDPNDESMNSPCQVQKW-----OLRLVYRKMLRTSEETI-----STVQEKQ 107
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  160 LEAOPF-----AHLT-----INATDIPSGSHKYSL-----SSWYHDR-GNAKISNM 199
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  108 QNISPLVNERGPQRYAAHITGTGRGSRNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNL 167
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  200 TFSNGKLIVNODGFYVLANICFRHHTSGDLATEYLQLMVYVTKTSIKIPSSHTLKKGG 259
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  168 HLRNGELVYHEKGFYIYSQYFRFQEEIKENTKNDKQMOYIYKYT-SYDPDILLKMSA 226
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  260 STKYWSGSEFHFYSINVGFFKLRSGEISIEVSNPSLDDPDADATYFGAFKY 313
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  227 RNSCMSKDAEGLYSIYQGGIFELKENDRIYVSTNEHLIDMDHEASFFGAFV 280
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 13
US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Ligand
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584.031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
```

```
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match      14.9%  Score 251.5; DB 3; Length 281;
Best Local Similarity 24.1%  Pred. No. 1.4e-17;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY  42 PAASRMEFALLGLGQVCSVALFEFFRAQMD--PRISEDGTHCIYRLRLHENDF 99
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  10 PSLGQTCVLIYFVYLLQSLCAVATYYFTNELKQMDKYSKSIACE-----LKED--- 61
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  100 QDTILESODTKLIPDSRRITQAFQAVQKELQHIYVGSQHTRAEKAVYDGSMDLAKRSK 159
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  62 -DSYWDPNDESMNSPCQVQKW-----OLRLVYRKMLRTSEETI-----STVQEKQ 107
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  160 LEAOPF-----AHLT-----INATDIPSGSHKYSL-----SSWYHDR-GNAKISNM 199
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  108 QNISPLVNERGPQRYAAHITGTGRGSRNTLSSPNSKNEKALGRKINSWSSRSGHSFLSNL 167
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  200 TFSNGKLIVNODGFYVLANICFRHHTSGDLATEYLQLMVYVTKTSIKIPSSHTLKKGG 259
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  168 HLRNGELVYHEKGFYIYSQYFRFQEEIKENTKNDKQMOYIYKYT-SYDPDILLKMSA 226
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
QY  260 STKYWSGSEFHFYSINVGFFKLRSGEISIEVSNPSLDDPDADATYFGAFKY 313
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB  227 RNSCMSKDAEGLYSIYQGGIFELKENDRIYVSTNEHLIDMDHEASFFGAFV 280
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 14
US-08-780-496-1
Sequence 1, Application US/08780496
Patent No. 6046048
GENERAL INFORMATION:
APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinpatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780.496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: P0978P1
REFERENCE/DOCKET NUMBER: 35,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-780-496-1
```

| | Query Match | 14.9%: | Score 251.5: | DB 3: | Length 281: |
|----|--|--------|--------------------|-------|-------------------------------------|
| | Best Local Similarity | 24.1%: | Pred. No. 1.4e-17: | | |
| | Matches | 71: | Conservative | 61: | Mismatches 117: Indels 45: Gaps 10: |
| Qy | 42 PAASRSMFVALGLGLGGVCSVALFFEFYRQMD--PNRISDEGTHCYIRILRLHENDF | 99 | | | |
| | : : : : : : : : : : : : : : : : : : : : : : : : : | | | | |
| Db | 10 PSLGTCVLIYFTYLLDLSCLVAYYYVFTNLRKQMDKYSKSGIACF-----LKED---- | 61 | | | |
| Qy | 100 QDTTLESODTKLIPDSCRRIKQAFQAVOKELQHTVYSGHRIAEKAMDGSLDLAKRSK | 159 | | | |
| | : : : : : : : : : : : : : : : : : : : : : : : : : | | | | |
| Db | 62 -DSYMDPNDDEESMNSPCMQVK-----QLRQLYRKMLRTSEBTI-----STVQEKQ | 107 | | | |
| Qy | 160 LEAQPF-----AHLT-----INATDIPSGSHKASL-----SSWYIDR-GMAKISMA | 199 | | | |
| | : : : : : : : : : : : : : : : : : : : : : : : : : | | | | |
| Db | 108 QNISPLVERERGQVRAAHITGTGRGNSNTLSPNSNKEKALIGRKISINWSSSRGSHSFLSL | 167 | | | |
| Qy | 200 TFSNCKLIYNQDGEFYVLIANICFRHHETSGDLATEVLDLQMYVTKRSIKIPSSHITLMKGG | 259 | | | |
| | : : : : : : : : : : : : : : : : : : : : : : : : : | | | | |
| Db | 168 HLRNELVIEHGGEFYIYSQYFRQOEIKETKNDKQWQVYIKYT-STYDPDILMKSA | 226 | | | |
| Qy | 260 STKYVSNSEEFYVGINVGFFPKRSGEEISILEVSNPSLLDPODATTYGAQKV | 313 | | | |
| | : : : : : : : : : : : : : : : : : : : : : : : : : | | | | |
| Db | 227 RNSCMSKDAEYLYLSYQGIFFELKENDRLFFYSVINEHLIDMDHESFFGAFVY | 280 | | | |

```

RESULT 15
US-08-883-086-10
; Sequence 10, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEO version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-10
Query Match 14.9%; Score 251.5; DB 4; Length 281
Best Local Similarity 24.1%; Pred. No. 1,4e-17;

```

| | Matches | 71, Conservative | 61, Mismatches | 117, Indels | 45, Gaps | 10, |
|----|---------|--|----------------|-------------|----------|-----|
| QY | 42 | PAASASMVALLIGLGQVCSVALFFPRAMD--PRISBDGTHCIIRLRLHENDAF | 99 | | | |
| Db | 10 | PSLGQTCVALIVFTVLDLSLCAVATVYFTTNLKKOMODYTSYGACF-----LLED--- | 61 | | | |
| QY | 100 | QDTLESODDTKLIPDSCRRIKQAFQAGVOKELQHTIVGSOHRIAEKRAMDGNLDAKRSK | 159 | | | |
| Db | 62 | -DSYMDPNDEESMNSPCWQVK-----QLROLVAKMLRTTSETI-----STVOEKO | 107 | | | |
| QY | 160 | LEAQEF-----AHLT-----INATDIPSGSHKVL-----SSWYHDR--GMAKISM | 199 | | | |
| Db | 108 | QNISFLVREKRGQRVAAHTTGRGNSNLTSSNSKNEKALGKKINSWESRSGHSLSL | 167 | | | |
| QY | 200 | TFSNGKLIVNODGFYYLVANICFRHHETSGDILATEYLDLMTVVTYKTSIKIPBSHTLMKCG | 259 | | | |
| Db | 168 | HLRNEELIVHEHGFYIYSQTYFRFOELIKENTKNDKCMQVOYLYKYT--SYRPIILMKSA | 226 | | | |
| QY | 260 | STKYSNGSEHFFYTSINWGFEKLKSGEETISLEVSNSPLDDPDODATYGAERK | 313 | | | |
| Db | 227 | RNSCMSKDEYGLYISYGGGIFELKENDLPIYSVTNEHLLIDMDHESFPGAFV | 280 | | | |

```
Search completed: July  8, 2002, 20:01:07
Job time: 4196 sec
```

| | | | | |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match | 14.98; | Score 251.5; | DB 4; | Length 281; |
| Best Local Similarity | 24.18; | Pred. NO. 1.4e-17; | | |

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 18:51:49 ; Search time 52.04 Seconds

(without alignments)
235.859 Million cell updates/sec

Title: US-09-865-363-13

Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEMG.....LDDPDADTYFGAFYVRDID 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swisprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1685 | 100.0 | 317 | 1 | TN11_HUMAN |
| 2 | 1417.5 | 84.1 | 316 | 1 | TN11_MOUSE |
| 3 | 251.5 | 14.9 | 281 | 1 | TN10_HUMAN |
| 4 | 248 | 14.7 | 291 | 1 | TN10_MOUSE |
| 5 | 189 | 11.2 | 281 | 1 | FASL_HUMAN |
| 6 | 184.5 | 10.9 | 279 | 1 | FASL_MOUSE |
| 7 | 176.5 | 10.5 | 261 | 1 | TNFS_BOVIN |
| 8 | 175.5 | 10.4 | 278 | 1 | FASL_RAT |
| 9 | 158.5 | 9.4 | 261 | 1 | TNFS_HUMAN |
| 10 | 152 | 9.0 | 260 | 1 | TNFS_MOUSE |
| 11 | 146 | 8.7 | 234 | 1 | TNFA_FELCA |
| 12 | 145 | 8.6 | 260 | 1 | TNFA_CAVPO |
| 13 | 141.5 | 8.4 | 235 | 1 | TNFA_MOUSE |
| 14 | 140.5 | 8.3 | 235 | 1 | TNFA_RABIT |
| 15 | 137 | 8.1 | 234 | 1 | TNFA_SHEEP |
| 16 | 134 | 8.0 | 233 | 1 | TNFA_MACFA |
| 17 | 134 | 8.0 | 240 | 1 | TN14_HUMAN |
| 18 | 133 | 7.9 | 233 | 1 | TN14_MOUSE |
| 19 | 133 | 7.9 | 233 | 1 | TNFA_CANFA |
| 20 | 133 | 7.9 | 233 | 1 | TNFA_HUMAN |
| 21 | 132.5 | 7.9 | 235 | 1 | TNFA_MCMU |
| 22 | 131.5 | 7.8 | 235 | 1 | TNFA_PERLE |
| 23 | 130.5 | 7.7 | 306 | 1 | TNFC_MOUSE |
| 24 | 130 | 7.7 | 233 | 1 | TNFA_MOUSE |
| 25 | 129.5 | 7.7 | 233 | 1 | TNFA_PAPPO |
| 26 | 129 | 7.7 | 233 | 1 | TNFA_MARMO |
| 27 | 128 | 7.6 | 234 | 1 | TNFA_HORSE |
| 28 | 126.5 | 7.5 | 233 | 1 | TNFA_BOVIN |
| 29 | 126 | 7.5 | 232 | 1 | TNFA_PIG |
| 30 | 122 | 7.2 | 133 | 1 | TNFA_CAVHI |
| 31 | 120 | 7.1 | 229 | 1 | TNFA_CEREL |
| 32 | 118 | 7.0 | 260 | 1 | TNFS_MOUSE |
| 33 | 117 | 6.9 | 233 | 1 | TNFA_FELCA |

| | | | | | | |
|----|------|-----|------|---|------------|--------------------|
| 34 | 117 | 6.9 | 244 | 1 | TNFC_HUMAN | 006643 homo sapien |
| 35 | 116 | 6.9 | 233 | 1 | TNFA_MACEU | 077764 macropus eu |
| 36 | 105 | 6.2 | 201 | 1 | TNFB_MACEU | 09x48 macropus eu |
| 37 | 97 | 5.8 | 1464 | 1 | CALL_HUMAN | P02452 homo sapien |
| 38 | 95 | 5.6 | 858 | 1 | V2A_CMVK | 086783 cucumber mo |
| 39 | 93 | 5.5 | 233 | 1 | TNFA_TRIUV | P79374 trichosurus |
| 40 | 92.5 | 5.5 | 205 | 1 | TNFB_HUMAN | P01374 homo sapien |
| 41 | 92.5 | 5.5 | 450 | 1 | YK22_YEAST | P36135 saccharomyc |
| 42 | 92 | 5.5 | 857 | 1 | V2A_CMVNT | 040977 cucumber mo |
| 43 | 90.5 | 5.4 | 858 | 1 | V2A_CMVNS | 039436 cucumber mo |
| 44 | 90.5 | 5.4 | 1694 | 1 | SN_MOUSE | 062230 mus musculu |
| 45 | 90 | 5.3 | 1460 | 1 | CALL_CANFA | 09x57 canis fam11 |

ALIGNMENTS

| RESULT | ID | STANDARD | PRT | AA |
|--------|--|-----------------|-----|-----|
| 1 | TN11_HUMAN | 014723; Q9P203; | 317 | AA. |
| AC | 014788; 014723; Q9P203; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update) | | | |
| DE | Tumor necrosis factor ligand superfamily member 11 (Receptor activator | | | |
| DE | of nuclear factor kappa B ligand) (RANKL) (TNF-related activation- | | | |
| DE | induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast | | | |
| DE | differentiation factor) (ODF). | | | |
| GN | TNFSF11 OR RANKL OR TRANCE OR OPGL. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=bone marrow, and peripheral blood; | | | |
| RX | MEDLINE=98032977; PubMed=9367155; | | | |
| RA | Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., | | | |
| RA | Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., | | | |
| RA | Galibert L.; | | | |
| RT | "A homologue of the TNF receptor and its ligand enhance T-cell growth | | | |
| RT | and dendritic-cell function."; | | | |
| RT | Nature 390:175-179(1997). | | | |
| RL | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Lymph node; | | | |
| RX | MEDLINE=98227661; PubMed=9568710; | | | |
| RA | Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., | | | |
| RA | Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., | | | |
| RA | Sullivan J., Hawkins N., Davy E., Capparello C., Eli A., Qian Y.-X., | | | |
| RA | Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., | | | |
| RA | Boyle W.J.; | | | |
| RT | "Osteoprotegerin ligand is a cytokine that regulates osteoclast | | | |
| RT | differentiation and activation."; | | | |
| RT | Cell 93:165-176(1998). | | | |
| RL | [3] | | | |
| RP | SEQUENCE OF 73-317 FROM N.A. | | | |
| RC | TISSUE=Thymocytes; | | | |
| RX | MEDLINE=97460112; PubMed=9312132; | | | |
| RA | Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., | | | |
| RA | Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., | | | |
| RA | Choi Y.; | | | |
| RT | "TRANCE is a novel ligand of the tumor necrosis factor receptor family | | | |
| RT | that activates c-Jun N-terminal kinase in T cells."; | | | |
| RT | J. Biol. Chem. 272:25190-25194(1997). | | | |
| RL | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 2). | | | |
| RC | TISSUE=Thymocyte; | | | |
| RX | MEDLINE=20175237; PubMed=10708588; | | | |
| RA | Nagai M., Kyakumoto S., Sato N.; | | | |
| RT | "Cancer cells responsible for humoral hypercalcemia express mRNA | | | |
| RT | encoding a secreted form of ODF/TRANCE that induces osteoclast | | | |
| RT | formation."; | | | |

```

RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
CC AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL
CC HYPERCALCEMIA OF MALIGNANCY
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
CC SECRETED (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/SODF; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NOSES BUT
CC WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC -1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF019047; AAB86811.1; -
DR EMBL: AF053712; AAC39731.1; -
DR EMBL: AF013171; AAC51762.1; -
DR EMBL: AB037599; BAA90488.1; -
DR MIM: 602642; -
DR InterPro: IPR003263; TNF_5.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00228; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR Prosite: PS50049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor; Alternative splicing
FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT TRANSMEM 48 68
FT DOMAIN 69 317 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 73 MISSING (IN ISOFORM 2).
FT CONFLICT 194 194 A -> G (IN REF. 3).
SO SEQUENCE 317 AA; 35478 MW; 766176446348097f CRC64;

```

```

Query Match 100.0%; Score 1685; DB 1; Length 317;
Best Local Similarity 100.0%; Pred. No. 7.4e-136; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 0;

```

```

DB 241 VYTKSIKIPSSHTLMKGSGTKYWSGNSFEHFYSINVGGFFKLRSGEISIEVSNPSLID 300
QY 301 PDDATYFAGAKVDID 317
DB 301 PDDATYFAGAKVDID 317
RESULT 2
TNF1_MOUSE STANDARD; PRT; 316 AA.
AC 035235; 035306;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE induced cytokine) (TRANCE) (osteoprotegerin ligand) (OPGL) (osteoclast
DE differentiation factor) (ODF) (osteoclastogenesis-inhibitory factor)
DE (OCIF).
GN TNFRSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hybridoma;
RX MEDLINE=97460112; PubMed=9312132;
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=98227661; PubMed=9568710;
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow stroma;
RX MEDLINE=98188248; PubMed=9520411;
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A.,
RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/Osteoclastogenesis-inhibitory factor and is identical
RT to TRANCE/RANKL.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic lymphoma;
RX MEDLINE=96032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougan W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Ikeda T.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL

```



```
CC PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
CC TRABECULAR BONE AND LUNG.
CC -1- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBOLO-
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH
CC OF NEONORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOECTROSTIS WITH
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN
CC HYPERTROPHIC CHONDROCYTES.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF053713; AAC40113.1; -
DR EMBL: AF013170; AAC71061.1; -
DR EMBL: AB008426; BAA25425.1; -
DR EMBL: AF019048; AAB86812.1; -
DR EMBL: AB036798; BAA37259.1; -
DR MGD: MGI:1100089; Tnfstf11
DR Interpro: IPR003263; TNF_5
DR Interpro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF_1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF_1.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine: Differentiation; Receptor; Glycoprotein; Transmembrane;
DR Signal-anchor.
DR TRANSMEM 1 48 CYTOPLASMIC (POTENTIAL).
DR TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
DR DOMAIN 1 48 (POTENTIAL).
DR CARBOHYD 70 316 EXTRACELLULAR (POTENTIAL).
DR CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
DR CONFLICT 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
DR CONFLICT 99 99 G->D (IN REF. 4).
DR SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;
SO
Query Match 84.1%; Score 1417.5; DB 1; Length 316;
Best Local Similarity 84.3%; Pred. No. 3.9e-113;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
OY 1 MRRASRDYTKYLRGSEEGGCGAPHEGRLH-APPAPAPHQPPAASRSMFALLGLGIGQ 59
DB 1 MRRASRDYTKYLRGSEEGGCGAPHEGRLH-APPAPAPHQPPAASRSMFALLGLGIGQ 60
OY 60 VVCSALFFYRAQMDPRISEDGTHCYRLRLHENAADFQDTLTESQDTKLIPDSCRI 119
DB 61 VVCSALFFYRAQMDPRISEDGTHCYRLRLHENAADFQDTLTESQDTKLIPDSCRI 118
OY 120 KOAFQAGVQKELQHYVSGHTRAEKAWDGSMDLAKRSKLEAPPAHLTTNATDIRSGS 179
DB 119 KOAFQAGVQKELQHYVSGHTRAEKAWDGSMDLAKRSKLEAPPAHLTTNATDIRSGS 178
OY 180 HKVSLSSVYHDSGNVAKISNMTFSNGKLIVNDGFEYLYANICFRHHETSGDLATEYQOLM 239
DB 179 HKVSLSSVYHDSGNVAKISNMTFSNGKLIVNDGFEYLYANICFRHHETSGDLATEYQOLM 238
OY 240 VVYVTKTSIKTSSHTLMKGGSTKTKWSGSEPHFYSINVGCFKLRSGEISTEVSNSPL 299
DB 239 VVYVTKTSIKTSSHTLMKGGSTKTKWSGSEPHFYSINVGCFKLRSGEISTEVSNSPL 298
OY 300 DPDDQATYFGAFKVDID 317
DB 299 DPDDQATYFGAFKVDID 316
RESULT 3
TNO_HUMAN STANDARD: PRT; 281 AA.
AC P50591;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN TNFSF10 OR TRAIL OR Apo2L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96111955; PubMed-8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
RT family that induces apoptosis."
RL Immunity 3:673-682(1995).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE-96278649; PubMed-8663110;
RA Pitti R.M., Masters S.A., Ruppert S., Donahue C.J., Moore A.,
RA Ashkenazi A.;
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
RT necrosis factor cytokine family."
RL J. Biol. Chem. 271:12687-12690(1996).
[3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
RX MEDLINE-20017054; PubMed-10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,
RA Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
RT complex with death receptor 5."
RL Mol. Cell 4:563-571(1999).
[4]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
RX PubMed-10542098;
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
RA Jones E.Y., Sreanion G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
RT specificity in apoptotic initiation."
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -1- FUNCTION: INDUCES APOPTOSIS.
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
CC AND PROSTATE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U37518; AAC50332.1; -
DR EMBL: U57059; AAB01233.1; -
DR MIM: 603596; -
```

DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR ProDom; PD008600; TNF_5; 1.
 DR SMART; SM00207; TNF_1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CytoKine; Transmembrane; Signal-anchor; Apoptosis; 3D-structure.
 KM DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
 SO SEQUENCE 281 AA; 32509 MW; DDAAAF78DAB2F6D CRC64;

Query Match 14.9%; Score 251.5; DB 1; Length 281;
 Best Local Similarity 24.1%; Pred. No. 3.7e-14;
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

DB 42 PAASSMEVALLGLGVCVALFFEFRAQMD--PRLSEDTGHCYIRLRHENDAF 99
 10 PSLGOTCVLIIVFTVLLSLCAVAVTYVFTNELKQMDKYSKSGIACF-----LKED--- 61
 QY 100 QDTLESODTKLIPDSRRIRKQAFQAVOKELQHTVSGOHTRAEKAMVDGSLDAKSK 159
 62 -DSYMDPNDEESMNSPCWQVKV-----QLROLVTKMLILTSETI-----STVQEKQ 107
 QY 160 LEAQP-----AHLT-----INATDIPSGSHKYSL-----SSWYHDR-GMAKISNM 199
 DB 108 QNISPLVREGRQORAAHITGRGNSNTLSSPNSKNAKLGKINSWESRGHFLSL 167
 QY 200 TFSNGKLIYNQDGFYLLVANICFRHETSGDLATEYLQMLVYVTKSTIKIPSSHTLMKG 259
 168 HIRNGELVHEKGFYIYQTFRFOEIEKENTKNDKQWQYIYKT--SYPPDILMKSA 226
 QY 260 STKYSGNSEPHFYSINVGCFKLSGGEISIEVSNPLDDPDQATYGFARKV 313
 227 RNSCWSKAEYGLYSIYGGIFELKENDRIEVSVTNEHLDMDEASFGAF 280
 DB

RESULT 4
 TN10_MOUSE STANDARD: PRT; 291 AA.
 ID TN10_MOUSE
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C.A., Goodwin R.G.;
 RT Identification and characterization of a new member of the TNF family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: INDUCES APOPTOSIS.
 CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U37522; AAC52345.1; -
 DR MGI; 107414; Tnfsf10.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR ProDom; PD008600; TNF_5; 1.
 DR SMART; SM00207; TNF_1; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CytoKine; Transmembrane; Signal-anchor; Apoptosis.
 KM DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 SO SEQUENCE 291 AA; 33477 MW; 3FECAB9F0D7D802 CRC64;

Query Match 14.7%; Score 248; DB 1; Length 291;
 Best Local Similarity 25.4%; Pred. No. 7.7e-14;
 Matches 79; Conservative 52; Mismatches 100; Indels 80; Gaps 13;

DB 46 RSMFVALLGLG-LGQVCSVALFFEFRAQMD--PRLSEDTGHCYIRLRHENDAF 102
 17 RMNVICIVLLQVLLQAVAVTYVFTNEMKQLODYSKIGLACFSK-----TDEDFWDS 71
 QY 103 TLESODTKLIPDSRRIRK-----OAFQ-----GAVQKEL 131
 DB 72 T-----DGETLNPCLQVNRKQLQLEEVTLTFPQDTISTPEKQSLTPPLRGGRPKQVA 127
 QY 132 QHTVSGOHTRAEKAMVDGSLDAKSKLEAPFAHLTINATDIPSGSHKYSLSWYHDR 191
 128 AHITGTR-RSNSALI-----PISKDGKTLGQ-----KIESMESSR 162
 QY 192 -GMAKISNMTSNGKLIYNQDGFYLLVANICFRHETSGDLATEYL-----QLMYV 242
 163 KGHSEFLNHVLFNGLVLEQEGLYIYQTFRFOEAD--ASKWVSKDKYRQOLVYI 220
 QY 243 TKTSTIKIPSSHTLMKGSGTKWYSGNSEPHFYSINVGCFKLSGGEISIEVSNPLDDPD 302
 DB 221 YKTT--SYPPDILMKSAKNSCWRDAEYGLYSIYGGIFELKKNRIRIVSVTNEHLMDD 279
 QY 303 QDATYGFARKV 313
 DB 280 QEASFGAF 290

RESULT 5
 FASL_HUMAN STANDARD: PRT; 281 AA.
 ID FASL_HUMAN
 AC P48023;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FAS antigen ligand (Apoptosis antigen ligand) (APL) (CD178 antigen).
 GN TNFSF6 OR APTL1G1 OR FASL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95105731; PubMed=7528780;
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T

| | |
|----|--|
| RT | "The mouse Fas-ligand gene is mutated in gld mice and is part of a |
| RT | TNF family gene cluster." |
| RL | Immunity 1:131-136(1994). |
| RN | (4) |
| RP | SEQUENCE FROM N.A. (ISOFORM FASL). |
| RC | STRAIN-BALB/C; |
| RA | Fenner M.H., Shioda T., Isselbacher K.J.; |
| RT | "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in |
| RT | two amino acids." |
| RL | Submitted (May-1996) to the EMBL/Genbank/DDBJ databases. |
| RN | [5] |
| RP | SEQUENCE FROM N.A. (ISOFORM FASLS). |
| RC | STRAIN-C3H; TISSUE-Spleen; |
| RX | MEDLINE=20021694; PubMed=10552956; |
| RA | Ayrollet E., D'Adamio F., Zollo O., Agostini M., Moraea R., |
| RA | Cannatille L., Migliorati G., Dellino D.V., Riccardi C.; |
| RT | "Cloning and expression of a short Fas ligand: A new alternatively |
| RT | spliced product of the mouse Fas ligand gene." |
| RL | Blood 94:3456-3467(1999). |
| RN | [6] |
| RP | CHARACTERIZATION OF VARIANT GLD. |
| RX | MEDLINE=96091792; PubMed=7495745; |
| RA | Hanne M., Peltsch M.C., Imtler W., Schroeter M., Lowin B., |
| RA | Rousseau M., Biron C., Renno T., French L., Tschoep J.; |
| RT | "Characterization of the non-functional Fas ligand of gld mice."; |
| RL | Int. Immunol. 7:1381-1386(1995). |
| CC | -I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT |
| CC | TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN |
| CC | CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. |
| CC | FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF |
| CC | PRIPIERIAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE |
| CC | T CELLS, OR BOTH. |
| CC | -I- SUBUNIT: HOMODIMER (PROBABLE). |
| CC | -I- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN. |
| CC | ISOFORM FASLS IS SOLUBLE. |
| CC | -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE |
| CC | PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS |
| CC | WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL |
| CC | INTERACTION. |
| CC | -I- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED |
| CC | LMPHOPLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE |
| CC | RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION. |
| CC | -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY. |
| CC | ----- |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - |
| CC | the European Bioinformatics Institute. There are no restrictions on its- |
| CC | use by non-profit institutions as long as its content is in no way |
| CC | modified and this statement is not removed. Usage by and for commercial |
| CC | entities requires a license agreement (see http://www.isb-sib.ch/announce/ |
| CC | or send an email to license@sib-sib.ch). |
| CC | ----- |
| DR | EMBL; U06948; AAA19780.1; . |
| DR | EMBL; U10984; AAA19778.1; . |
| DR | EMBL; S76752; AAB33780.1; . |
| DR | EMBL; S76895; AAB02915.1; . |
| DR | EMBL; AF119335; AAD52106.1; . |
| DR | HSSP; P01375; 4TSV. |
| DR | MGI; MGI:99255; Tnfrsf6. |
| DR | InterPro; IPR003263; TNF_5. |
| DR | InterPro; IPR003636; TNF_abC. |
| DR | InterPro; IPR004478; TNF_family. |
| DR | Pfam; PF00229; TNF_1. |
| DR | ProDom; PD002012; TNF_abC; 1. |
| DR | ProDom; PD008600; TNF_5; 1. |
| DR | SMART; SM00207; TNF_1. |
| DR | PROSITE; PS00251; TNF_1; 1. |
| DR | PROSITE; PS00049; TNF_2; 1. |
| KW | Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis; |
| KW | Disease mutation; Alternative splicing. |
| FT | DOMAIN 1 78 |
| FT | CDYTOPLASMIC (POTENTIAL). |
| FT | SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). |
| FT | EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 79 100 |
| FT | DOMAIN 101 279 |

| FT | DOMAIN | 4 | 69 | PRO-RICH. |
|---|---|--|-----------------|---|
| FT | DOMAIN | 45 | 51 | POLY-PRO. |
| FT | DISULFID | 200 | 231 | BY SIMILARITY. |
| FT | CARBOHYD | 117 | 117 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 182 | 182 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 248 | 248 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 258 | 258 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VASPEPTIC | 1 | 210 | MISSING (IN ISOFORN FASTS). |
| FT | VARIANT | 184 | 184 | T -> A (IN STRAIN BALB/C). |
| FT | VARIANT | 218 | 218 | E -> G (IN STRAIN BALB/C). |
| FT | VARIANT | 273 | 273 | F -> L (IN GUD; ABOLISHES BINDING OF FAST TO ITS RECEPTOR). |
| SO | SEQUENCE | 279 AA; | 31442 MW; | 37972E3728E0A1CA CRC64; |
| Query Match 10.98; Score 184.5; DB 1; Length 279; | | | | |
| Best Local Similarity 21.78; Pred. No. 1.8e-08; | | | | |
| Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps | | | | |
| OY | 13 | RGESEMGGPGAPCEGJLHAPPPAPHPQ----- | -PASRSMEVALLGLL | 57 |
| Db | 38 | RGRPGRRRRRRRRPVSLPRPSQPLRLPLRLPKKDDHNTNMLPVYEFMVLLVALQKML | | 97 |
| OY | 58 | GQVVCVALEFFRYFAQMDPNRKISEDGTHCIYLRILRLHENDAFODTTLSEQDTKLIPDSCR | | 117 |
| Db | 98 | G-----MYOLFHL----- | | 105 |
| OY | 118 | RIKQAFQGVQKQELQHT--VGSQHRA---EKMVVGSMYLDLAKRSKLEAOPFAHLITNA | | 172 |
| Db | 106 | -----OKELAEIRFTTNSLAKVSEKQIAPNS-----TPSKKRPRAVHNLGN- | | 150 |
| OY | 173 | TDIPSGSHKYSLS-SWYHDSGMAKISMPFNSGKLIVNDGFYUYLVANICFRHHETSGDL | | 231 |
| Db | 151 | -----PHSRSDIPLEWEDDTGTALISGVKKKGLVINEGTGLTFVYSKYVFFRGOSCN-- | | 201 |
| OY | 232 | ATEYQLQMVVYVTKTSIKIPSSHILMKSGSKYMSGNSEFFHYSINVGEPFKLRSGEIS | | 291 |
| Db | 202 | -NQPNHKKVYKRN--KYPEDLVLMKKRLNLTCT-TGQIWAHSYLGAVFNLTSDHLIV | | 257 |
| OY | 292 | EVSNPSLDDPDQATVFGAFKRV | 313 | |
| Db | 258 | NLSQSLINFEESKTFPGLYKL | 279 | |
| RESULT 7 | | | | |
| TFNS_BOVIN | TFNS_BOVIN | STANDARD; | PRT; | 261 AA. |
| AC | PS1749; | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen GP39). | | | |
| GN | TFNSFS OR CD40LG OR CD40L. | | | |
| OS | Canis taurus (Bovine). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; | | | |
| OC | Bovidae; Bovinae; Bos. | | | |
| OX | NCBI_TaxID=9913; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | TISSUE=Blood; | | | |
| RC | MEDLINE=96006582; PubMed=7590981; | | | |
| RA | Mertens B.E.L.C., Muriuki M., Gaidulis L.; | | | |
| RT | "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha."; | | | |
| RL | Immunogenetics 42:430-431(1995). | | | |
| CC | -I- FUNCTION: ACTIVATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4. | | | |
| CC | INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY). | | | |
| CC | -I- SUBUNIT: HOMOTRIMER. | | | |
| CC | -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY). | | | |

```

CC -1 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 248469; CAA8363.1; .
DR HSSP; P29965; IALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 22
FT TRANSMEM 23 46
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT POTENTIAL.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 47 261
FT DISULFID 178 218
FT CARBOHYD 240 240
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 261 AA: 29242 MW: 84915FEFB30A787ED CRC64;

Query Match 10.5%; Score 176.5; DB 1; Length 261;
Best Local Similarity 24.2%; Pred. No. 7.9e-08;
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

OY 33 PPPAPHPAPASRSMFVALLGLG-GOVCSVALFFFRQMDPRISDGHCIYRL 91
DB 8 PPSRVATGCPVSMKIFMYLLVFLITQMGSLFAVYLHRLD-KIIDE-----R 57
OY 92 RHENANDODT--TLESODTKLIPDSCKRIKQAFQAVOKELQHTVSGOHTRAEKAVDG 149
DB 58 NHHEDFVEMKTIQRNCNKGESLSLNCCEIRSFEDLVKDIQO---KKEVKKKKKEFE- 112
OY 150 SWDLAKRSKSLKLEAPFAHLTINATDIPSGSHKVSLSWYHGRMAKIN--MTFENGR-L 206
DB 113 -----MHKGDPEQIAIAIVISAS-----SKTTSVLQW-APRGYTTLSNNLTLENGKOL 161
OY 207 IVNODGFYLYLVANICFRHHTSGDLATEYLDLMVYVTKTSIKIP--SSHTLKKGGSTKYW 264
DB 162 AVKRGGFYIYTOVFECSNR-----ETLSQAPFIASLCKSPSGSRILLRANHTH-- 212
OY 265 SGNSEFHYSTINVGFFFLRSGEISIEVSNPSLLDPDQATYFGAFKV 313
DB 213 SSSKPCGQSIHLGQVFLQSGASVFNVTDPQVSHGTGFTSFLKL 261

RESULT 8
FASTL_RAT STANDARD: PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FAS antigen ligand
CN TNFSF6 OR AP11LGI OR FASL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the fas ligand, a novel member
RT of the tumor necrosis factor family.";

```

```

RL Cell 75:1169-1178(1993).
CC -1 FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -1 SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -1 INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03470; AAC52129.1; .
DR HSSP; P01375; AFSV.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
KW CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 77
FT TRANSMEM 78 99
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 100 278
FT PRO-RICH.
FT DOMAIN 45 58
FT POLY-PRO.
FT DISULFID 199 230
FT BY SIMILARITY.
FT CARBOHYD 116 116
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA: 31140 MW: 2898E18A862CEAC6 CRC64;

Query Match 10.4%; Score 175.5; DB 1; Length 278;
Best Local Similarity 20.3%; Pred. No. 1e-07;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

OY 21 GPGAPHEGPHLAPPAPHPAPASRSM-----FWALLGLGL 57
DB 39 GPGGRPPPP--PPPPSPPLPPSPQPLPLPLKKNIEMLPVFFWLVALVGMGL 96
OY 58 GOVCSVALFFERYAKQMDPRISDGHCIYRIIRLHENDPDDTLESODTKLIPSCR 117
DB 97 G-----WQFLQKELAELEFETNHSI-RVSSFEKQIANDSTPBTYKPPSV----- 143
OY 118 RIKQAFQAVOKELQHTVSGOHTRAEKAVDGSWDLAKRSKLEAQFAHLTINATDIPS 177
DB 144 -----
OY 178 GSHKVSLSWYHGRMAKISMTFNSCKLLVNDGFYLYLVANICFRHHTSGDLATEYLD 237
DB 152 -SRSIPL-EMEDYTGALLIGVKKKGGLVINEAGLVFVYSKYVFGQSCN---SQPLS 205
OY 238 LMVYVTKTSIKIPSSHLMKGGSTKYWGSNSEFHYSTINVGFFFLRSGEISIEVSNPS 297
DB 206 HKYVM--RNKKYGGDLVMEKKLNCIT-TGQIAHSSYLGAVFNLTVDHLVYNISQLS 262

```

| DB | LINEESTFOLGVL | 278 |
|------------|--|-----------------------------------|
| Y | 298 | LDPEODATYFGCAFKV 313 |
| Y | 1 | 1:1:1:1:1 |
| DB | 263 | LINEESTFOLGVL 278 |
| RESULT | 9 | |
| TNFS_HUMAN | STANDARD: | PRT: 261 AA. |
| AC | P29965: | |
| DT | 01-APR-1993 | (Rel. 25, Last sequence update) |
| DT | 01-APR-1993 | (Rel. 25, Last sequence update) |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) |
| DE | CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell antigen gp39) (CD154 antigen). | |
| DE | TNFSF5 OR CD40LG OR CD40L OR TRAP. | |
| OS | Homo sapiens (Human). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| OC | NCBI_TaxID:9606; | |
| RN | SEQUENCE FROM N.A. | |
| RX | MEDLINE=93076854; PubMed=1280226; | |
| RT | Graf D., Korthauer U., Mages H.W., Senger G., Krocsek R.A.; | |
| RL | "Cloning of TRAP, a ligand for CD40 on human T cells."; | |
| RL | Eur. J. Immunol. 22:3191-3194(1992). | |
| RN | SEQUENCE FROM N.A. | |
| RX | MEDLINE=93049181; PubMed=1385114; | |
| RA | Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N., | |
| RA | Bresch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A., | |
| RA | Aruffo A.; | |
| RT | "The human T cell antigen gp39, a member of the TNF gene family, is a ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-stimulatory activity."; | |
| RL | EMBO J. 11:4313-4321(1992). | |
| RN | SEQUENCE FROM N.A. AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235. | |
| RX | MEDLINE=93145330; PubMed=7678782; | |
| RA | Aruffo A., Farrington M., Hollenbaugh D., Li X., Malatovich A., | |
| RA | Nonoyama S., Bajorth J., Grosmaire L.S., Stenkamp R., Neubauer M., | |
| RA | Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.; | |
| RT | "The CD40 ligand, gp39, is defective in activated T cells from patients with X-linked hyper-Igm syndrome."; | |
| RL | Cell 72:291-300(1993). | |
| RN | SEQUENCE FROM N.A. | |
| RX | MEDLINE=93094757; PubMed=1281209; | |
| RA | Spitigs M.K., Armitage R.J., Stroockline L., Clifford K.N., | |
| RA | Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.; | |
| RT | "Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion."; | |
| RL | J. Exp. Med. 176:1543-1550(1992). | |
| RN | SEQUENCE FROM N.A. | |
| RX | MEDLINE=93138085; PubMed=7678552; | |
| RA | Gauchat J.F.M., Aubry J., Mazzei G.J., Life P., Jomotte T., Elson G., | |
| RA | Bonnefoy J.Y.; | |
| RT | "Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression by factors controlling Ige production."; | |
| RL | FEBS Lett. 315:259-266(1993). | |
| RN | SEQUENCE FROM N.A. | |
| RA | Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H., | |
| RA | Matsuda I.; | |
| RT | Submitted (FEB-1995) to the EMBL/GenBank/DBD databases. | |
| RN | X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261. | |
| RX | MEDLINE=96131874; PubMed=8589998; | |
| RA | Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S., | |
| RA | Chess L., Thomas D.; | |
| RT | "A crystal structure of an extracellular fragment of human CD40 ligand."; | |
| RL | Structure 3:1031-1039(1995). | |
| RN | 3D-STRUCTURE MODELING OF COMPLEX WITH CD40. | |
| RX | MEDLINE=98266353; PubMed=9605317; | |
| RA | Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M., | |
| RA | Zheng Z., Naismith J.H., Thomas D.; | |
| RT | "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40."; | |
| RL | Protein Sci. 7:1124-1135(1998). | |
| RN | VARIANTS HIGM1 ARG-36 AND GLY-140. | |
| RX | MEDLINE=93156839; PubMed=7679206; | |
| RA | Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M., | |
| RA | Malcolm S., Uzzio A.G., Notarangelo L.D., Levinsky R.J., | |
| RA | Krocsek R.A.; | |
| RT | "Defective expression of T-cell CD40 ligand causes X-linked immunodeficiency with hyper-Igm."; | |
| RL | Nature 361:539-541(1993). | |
| RN | VARIANT HIGM1 GLU-123. | |
| RX | MEDLINE=93156840; PubMed=8094231; | |
| RA | Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A., | |
| RA | de Saint Basile G.; | |
| RT | "CD40 ligand mutations in X-linked immunodeficiency with hyper-Igm."; | |
| RL | Nature 361:541-543(1993). | |
| RN | VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227. | |
| RX | MEDLINE=93174270; PubMed=7679801; | |
| RA | Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A., | |
| RA | Galliani S., Matluano E., Fasth A., Andersson B., Zegers B.J.M., | |
| RA | Simoneaux D.K., Fanslow W.C., Belmont J.W., Spitigs M.K.; | |
| RT | "CD40 ligand gene defects responsible for X-linked hyper-Igm syndrome."; | |
| RL | Science 259:990-993(1993). | |
| RN | VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144. | |
| RX | MEDLINE=95233438; PubMed=7717401; | |
| RA | Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnani D., | |
| RA | Galliani S., Matluano E., Fasth A., Andersson B., Zegers B.J.M., | |
| RA | Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airo P., | |
| RA | Plebani A., Verzoni P., Notarangelo L.D.; | |
| RT | "Characterization of nine novel mutations in the CD40 ligand gene in patients with X-linked hyper Igm syndrome of various ancestry."; | |
| RL | Am. J. Hum. Genet. 56:898-906(1995). | |
| RN | VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219. | |
| RX | MEDLINE=96133533; PubMed=8550833; | |
| RA | Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O., | |
| RA | Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.; | |
| RT | "A single strand conformation polymorphism study of CD40 ligand. Efficient mutation analysis and carrier detection for X-linked hyper Igm syndrome."; | |
| RL | J. Clin. Invest. 97:196-201(1996). | |
| RN | VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL. | |
| RX | MEDLINE=97295077; PubMed=9150729; | |
| RA | Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M., | |
| RA | Yata J.-I., Och H.D.; | |
| RT | "Mutations of the CD40 ligand gene in 13 Japanese patients with X-linked hyper-Igm syndrome."; | |
| RL | Hum. Genet. 99:624-627(1997). | |
| CC | -I- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4. | |
| CC | INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING. | |
| CC | -I- SUBUNIT: HOMOTRIMER. | |
| CC | -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM. | |
| CC | -I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+ T-LYMPHOCYTES. | |
| CC | -I- DISEASE: DEFECTS IN TNFSF5 ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1), AN IMMUNOGLOBULIN ISOTYPE SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE) | |

CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
CC PNEUMOCYSTIS CARINITI PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLSCENCE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME=CD40Lbase;
CC NOTE-European CD40L defect database (mutation db);
CC WWW="http://www.expasy.org/cd40lbase/";
CC FTP="ftp://ftp.expasy.org/databases/cd40lbase";
CC -1- DATABASE: NAME=PROV: NOTE-CD guide CD154 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd154.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X68550; CAA48554.1; -;
CC DR EMBL: 215017; CAA78737.1; -;
CC DR EMBL: X67878; CAA48077.1; -;
CC DR EMBL: L07414; AAA35662.1; -;
CC DR EMBL: D31797; BAA06599.1; -;
CC DR EMBL: D31793; BAA06599.1; JOINED.
CC DR EMBL: D31794; BAA06599.1; JOINED.
CC DR EMBL: D31795; BAA06599.1; JOINED.
CC DR EMBL: D31796; BAA06599.1; JOINED.
CC DR PIR: S25684; S25684.
CC DR PIR: S26694; S26694.
CC DR PIR: S28017; S28017.
CC DR PIR: S28852; S28852.
CC DR PIR: JH0793; JH0793.
CC DR PDB: 1ALY; 17-SEP-97.
CC DR MIM: 308230; -;
CC DR InterPro: IPR003263; TNF_5.
CC DR InterPro: IPR000478; TNF_family.
CC DR Pfam: PF00229; TNF_1.
CC DR ProDom: PD008600; TNF_5; 1.
CC DR SMART: SM00207; TNF_1.
CC DR PROSITE: PS00251; TNF_1; 1.
CC DR PROSITE: PS50045; TNF_2; 1.
CC KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
CC Antigen; Disease mutation; Polymorphism.
CC FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 47 261 EXTRACELLULAR (POTENTIAL).
CC FT DISULFID 178 218 POTENTIAL.
CC FT CARBOHYD 240 240 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT VARIANT 36 36 M->R (IN H1GM1).
CC FT VARIANT 123 123 /FTID-VAR.007513.
CC FT VARIANT 126 126 A->E (IN H1GM1).
CC FT VARIANT 126 126 /FTID-VAR.007514.
CC FT VARIANT 126 126 V->A (IN H1GM1).
CC FT VARIANT 128 129 /FTID-VAR.007515.
CC FT VARIANT 128 129 SE->RG (IN H1GM1).
CC FT VARIANT 140 140 /FTID-VAR.007516.
CC FT VARIANT 140 140 W->C (IN H1GM1).
CC
CC Query Match 9.4%; Score 158.5; DB 1; Length 261;
CC Best Local Similarity 24.5%; Pred. No. 2.7e-06;
CC Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;
QY 45 SRSFVALTGLT-GGVVSVAFLEFFRAQMDPRISDGHCIYRLRLHENDPQDT- 102
QY 20 SMKIFMLTYFLITOMIGSLNPAVYLHRRID-KIIDE-----RNLDHEDVEFKTI 69
QY 103 -TLESQDKLIPDSGRIRKAFQAVOKELQHIYGSCHIRAKAMVDGWSLDLAKRSKLE 161
QY 70 QRCWTGRSRLSLNCEIKSOFEGFV-KDLM-----LKEETKKKNSP-EMQKGDQ-N 119

QY 162 AQPFAHLTINATDIPSGSHKYSLSWYHRCMAKISN--MTFSNGK-LIYNQGSFYLYA 218
QY 120 PQAIAHYISES-----SKTTSVLQW-AEKGYTMSNNVLLENGKOLTYKROGLYYIA 173
QY 219 NICEFHHTSGDLATEYLQIAVYVTKTSIKIPS--SHTLMGSGSTKYWSGSEFHFYSIN 276
QY 174 QVTFCSNRNEASSQAP-----FIASLCIKSPGFEHILRAANTH--SSAKPCGGOSIH 224
QY 277 VGGFFKLRSGEISIEVSNPLDPPDDATYFGAFKV 313
QY 225 LGVGFELQPGASVFNVTDPDSQVSHGTGFTSGFLKL 261
DB
RESULT 10
TNFS_FELCA
ID TNFS_FELCA STANDARD; PRT; 260 AA.
AC 097605;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C40_1lgand (CD154 antigen).
GN TNFS3 OR CD40LG OR CD40L.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Hosie M.J., Willett B.J.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF079105; AAD02954.1; -;
CC DR HSSP: P29965; 1ALY.
CC DR InterPro: IPR003263; TNF_5.
CC DR InterPro: IPR000478; TNF_family.
CC DR Pfam: PF00229; TNF_1.
CC DR ProDom: PD008600; TNF_5; 1.
CC DR SMART: SM00207; TNF_1.
CC DR PROSITE: PS00251; TNF_1; 1.
CC DR PROSITE: PS50045; TNF_2; 1.
CC KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 47 260 EXTRACELLULAR (POTENTIAL).
CC FT DISULFID 177 217 POTENTIAL.
CC FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT SEQUENCE 260 AA; 28727 MW; 349FA0391FB7B932 CRC64;
CC
CC Query Match 9.0%; Score 152; DB 1; Length 260;
CC Best Local Similarity 23.4%; Pred. No. 9.5e-06;
CC Matches 68; Conservative 55; Mismatches 121; Indels 46; Gaps 14;
QY 32 APPPAHPDPAASRSMFVALLGLT-GGVVSVAFLEFFRAQMDPRISDGHCIYRI 90

```

Db      9 APR59AP--GPPVSKITMYLTITVLTOMIGSALFANYLRRDD--KIEE----- 56
Oy      91 LRLHENADEFODTLESQ--DTKLIPDSCRIKQAFQAVORELOHIVSGHIREKAMVD 148
Db      57 RNLVDFEYFMKTLQCNKGEGALSLNCEELKSREAF-----LKIMLNKTEKKEKNA- 111
Oy      149 GSWMLDARKSLKEAPFHLITNADIDPSGSHKVSLSWYHDRCNAKISN--MFESNGK- 205
Db      112 -----MKGGDPPVAAHVISEAS-----SSTASVLQW-APKGYTTISNLTVLNKGQ 159
Oy      206 LIVNODGFYLYIYANICFRHETSGLATEYLQLMVYTKTSIKIP--SSHTLMKGGSTKY 263
Db      160 LAVKROGLIYIYAQVTFPCSNRRASSQAP-----FISLCHSPSSGSERYLLRANMR- 211
Oy      264 WSGNSEFHFYSINVGFFKLRSGEISIEVNSPLDDPDQATYTGAFKV 313
Db      212 -SSKPCGQGSITLGGVELHFGASVFVNVDPDPSQVSHGTGFTSGLKL 260

RESULT 11
TNFA_CAVPO STANDARD: PRT: 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DUNKIN-HARTLEY;
RX MEDLINE=97462215; PubMed=9316485;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
   factor-alpha.";
RL Am. J. Physiol. 273:1524-1530(1997).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
   WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
   CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
   CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
   OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
   CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
   CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
   EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
   PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
   CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
   AND MAINTNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U39839; AAB06492.1; -
CC EMBL: U77036; AAB19210.1; -

```

```

DR      HSP: P06804; 2TNF.
DR      InterPro: IPR003636; TNF_abc.
DR      InterPro: IPR000478; TNF_family.
DR      Pfam: PF00229; TNF_1.
DR      PRINTS: PR01234; TNECROSISFCT.
DR      PRODOM: PD002012; TNF_abc; 1.
DR      SMART: SM00207; TNF_1.
DR      PROSITE: PS00251; TNF_1; 1.
DR      PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Cytotoxicity; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1
FT CHAIN 80 234
FT TRANSMEM 36 56
FT DISULFID 147 178
FT SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 8.7%; Score 146; DB 1; Length 234;
Best Local Similarity 25.4%; Pred. No. 2,7e-05;
Matches 50; Conservative 30; Mismatches 75; Indels 42; Gaps 8;

Oy      134 IYSGHITAEKAMVDGSLDLAKRSKLEA-----QPFHLITNADIDPSGSHKVSLS 186
Db      55 VIGPQ--REDFSSGPPRPILAQTLLRSASQNDKRVAAHVAN-----QQAEEELQ 105
Oy      187 WYHDRGMAKISN-MTFSGKLIVNODGFYLYANICFRHETSGLATEYLQLMVYTKT 245
Db      106 WLSKRAMNLLNMGMLSDNQLVPSDGLIYLSQVLFK-----GQGCPSYLLTHTVSRL 160
Oy      246 SIKIPSSHFLM-----KGGSTKYWSGNSFEHFYSINVGFFKLRSGEISIEV 293
Db      161 AVSYPERKVNLLSAIKSPQCKETPEGAERKPW-----YEPYILGGVFLQKGDRLSAEV 213
Oy      294 SNPSLDD-PDQATYFG 309
Db      214 NLPQYLDPRADSSQIYFG 230

RESULT 12
TNF5_CANFA STANDARD: PRT: 260 AA.
AC O97626;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CD40 ligand.
GN TNF5F5 OR CD40LG OR CD40L.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willett B.J.;
RT "Adjuvant properties of canine CD40L.";
RL Submitted (A05-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
   STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
   INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
   EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF086711; AAD04375.1; -

```



```
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U06950: AAA18594.1; -.
DR EMBL: M13049: AAA40457.1; -.
DR EMBL: M11731: AAA40458.1; -.
DR EMBL: Y00467: CAA68530.1; -.
DR EMBL: X02611: CAA26457.1; -.
DR EMBL: M20155: AAA40462.1; ALT_SEQ.
DR EMBL: M38296: AAA40459.1; -.
DR EMBL: D84196: BAA19512.1; -.
DR EMBL: D84194: BAA19512.1; JOINED.
DR EMBL: D84195: BAA19512.1; JOINED.
DR EMBL: D84197: BAA19513.1; JOINED.
DR EMBL: D84198: BAA19513.1; JOINED.
DR PIR: A23127: QMMSN.
DR PIR: A22908: A22908.
DR PIR: A25164: A25164.
DR PIR: A27303: A27303.
DR PIR: A34251: A34251.
DR PIR: S03791: S03791.
DR PDB: 2TNF: 12-OCF-99.
DR MCD: MCI104798: TNF.
DR InterPro: IPR003636: TNF_abc.
DR InterPro: IPR000478: TNF_family.
DR Pfam: PF00229: TNF.
DR PRINTS: PRO1234: TNFROSISFCT.
DR PRODOM: PD002012: TNF_abc.
DR SMART: SM00207: TNF.
DR PROSITE: PS00251: TNF_1; 1.
DR PROSITE: PS00049: TNF_2; 1.
DR Cycloline: Cyclo toxin; Transmembrane; Glycoprotein; Signal-anchor;
KW 3D-structure.
FT PROPEP 1 79
FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 148 179
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .).
FT CONFLICT 231 231 G->R (IN REF. 3 AND 4).
SQ SEQUENCE 235 AA; 25895 MW; 16DD2A9676D66C5D CRC64;
```

Query Match 8.4%; Score 141.5; DB 1; Length 235;
Best Local Similarity 25.9%; Pred. No. 6.5e-05;
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

```
Oy 163 QPFAHLLTNATDIPSGSHKYSLS-SWYHNRGAKTSN-WTFENGKLIYNQDFFYLXANI 220
Db 90 KPAHVAVN-----HQVEQDLEWLSQRANALLANGMDLNDLVVPADSLYLVYGV 141
Oy 221 CRHHETSGDLATEYLQILMNVYTK-----TSIKIPSSHTLMKSGSTKYWSGNS 268
Db 142 LFK-----GGGCPDYVLTLHTYVSRAISYQEKVNLISAVKSCPPDTPGALAKFW----- 192
```

```
Oy 269 EFHYSINVGFEEKIRSGEISIEVSNPSLID-PDQATYTG 309
Db 193 --YEPIYGVGFQLEKGDQLSAEVNLPKLYDFAESEGVYEG 231

RESULT 14
ID TNFA_RABIT STANDARD; PRT; 235 AA.
AC P04924;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
DE TNF OR TNFA.
GN Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; PubMed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Nedospasov S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219712; PubMed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; PubMed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:149-156(1986).
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS. IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M12845: AAA31486.1; -.
DR EMBL: M12846: AAA31482.1; -.
DR EMBL: M60340: AAA31484.1; -.
DR PIR: A25451: A25451.
DR PIR: A25454: A25454.
```


Tue Jul 9 13:21:07 2002

us-09-865-363-13.rsp

Page 14

QY .232 ATEYLQAWVYTKTSIKIPSSHLMKGGSTKRYMSGNSEFPFYHINQGFKKLSGEIS 291
 Db 161 AVSY-QTRVNTLL-SKIKSPCHRETLLEGAKPW-----YEPYGGGVFQLEKGRDLSA 211
 QY 292 EYVSNPSLLD-PDQATYFNG 309
 Db 212 ETLNPEYLDYAESGVYFNG 230

Search completed: July 8, 2002, 18:51:50
Job time: 17488 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2002, 19:52:38 ; Search time 119.9 Seconds
(without alignments)
457,376 Million cell updates/sec

Title: US-09-865-363-13
Perfect score: 1685
Sequence: 1 MRASRDYTYTLRGSEBMG.....LDPDDATYGAFAKVRDID 317

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL.19:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_prodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|-------------------------|
| 1 | 1422 | 84.4 | 270 | 4 Q96Q17 | Q96Q17 homo sapien |
| 2 | 1409 | 83.6 | 313 | 11 Q9RIY0 | Q9RIY0 mus musculu |
| 3 | 1396.5 | 82.9 | 318 | 11 Q9SE82 | Q9SE82 ratu mus musculu |
| 4 | 1271 | 75.4 | 287 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 5 | 909 | 53.9 | 199 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 6 | 262 | 15.5 | 53 | 11 Q9JJK8 | Q9JJK8 mus musculu |
| 7 | 240.5 | 14.3 | 214 | 13 Q9DD25 | Q9DD25 brachydanto |
| 8 | 216.5 | 12.8 | 267 | 13 Q9DD25 | Q9DD25 brachydanto |
| 9 | 200 | 11.9 | 282 | 6 Q9BEA8 | Q9BEA8 sus scrofa |
| 10 | 200 | 11.9 | 282 | 6 Q9BEA8 | Q9BEA8 sus scrofa |
| 11 | 199 | 11.8 | 280 | 6 Q9MYI6 | Q9MYI6 macaca neme |
| 12 | 186 | 11.0 | 280 | 6 Q9BDM5 | Q9BDM5 macaca neme |
| 13 | 184.5 | 10.9 | 280 | 6 Q9BDM5 | Q9BDM5 macaca neme |
| 14 | 182.5 | 10.8 | 280 | 6 Q9BDN3 | Q9BDN3 cercocebus |
| 15 | 169.5 | 10.1 | 261 | 6 Q9BDN3 | Q9BDN3 callithrix |
| 16 | 167.5 | 9.9 | 261 | 6 Q9BDM3 | Q9BDM3 aotus trivi |

| | | | | | |
|----|-------|-----|-----|-----------|----------------------|
| 17 | 155.5 | 9.2 | 261 | 6 Q9BDC7 | Q9BDC7 macaca mula |
| 18 | 155 | 9.2 | 272 | 13 Q9IBD8 | Q9IBD8 gallus gall |
| 19 | 145.5 | 8.6 | 239 | 11 Q9QYH9 | Q9QYH9 mus musculu |
| 20 | 145 | 8.6 | 174 | 4 Q95150 | Q95150 homo sapien |
| 21 | 144 | 8.5 | 232 | 11 Q95853 | Q95853 mus musculu |
| 22 | 143 | 8.5 | 240 | 6 Q9BDM7 | Q9BDM7 macaca neme |
| 23 | 139.5 | 8.3 | 215 | 11 Q99ND1 | Q99ND1 lamasciuru |
| 24 | 137.5 | 8.2 | 156 | 11 Q91ZL4 | Q91ZL4 sigmodon hl |
| 25 | 136 | 8.1 | 234 | 6 Q98320 | Q98320 capra hircu |
| 26 | 134.5 | 8.0 | 310 | 11 Q9JMI0 | Q9JMI0 marmota mon |
| 27 | 134 | 8.0 | 157 | 4 Q43647 | Q43647 homo sapien |
| 28 | 134 | 8.0 | 204 | 4 Q96LD2 | Q96LD2 homo sapien |
| 29 | 133 | 7.9 | 149 | 6 Q97543 | Q97543 aotus nancy |
| 30 | 133 | 7.9 | 191 | 6 Q9MYZ2 | Q9MYZ2 capra hircu |
| 31 | 133 | 7.9 | 232 | 4 Q9UVI3 | Q9UVI3 homo sapien |
| 32 | 131.5 | 7.8 | 216 | 11 Q70332 | Q70332 mesocricetu |
| 33 | 130 | 7.7 | 217 | 11 Q9ERG6 | Q9ERG6 peromyscus |
| 34 | 128 | 7.6 | 234 | 6 Q9TTJ3 | Q9TTJ3 equus cabal |
| 35 | 127.5 | 7.6 | 217 | 6 Q9BEC5 | Q9BEC5 tenrec ecau |
| 36 | 127.5 | 7.6 | 235 | 11 Q9J127 | Q9J127 ratu mus norv |
| 37 | 127.5 | 7.6 | 235 | 11 Q9J126 | Q9J126 marmota mon |
| 38 | 127.5 | 7.6 | 310 | 11 Q9JMI1 | Q9JMI1 marmota mon |
| 39 | 126 | 7.5 | 149 | 6 Q97538 | Q97538 aotus vocif |
| 40 | 126 | 7.5 | 149 | 6 Q9TTG8 | Q9TTG8 aotus nigri |
| 41 | 125 | 7.4 | 216 | 6 Q9BEC9 | Q9BEC9 ochotona pr |
| 42 | 124 | 7.4 | 250 | 6 Q9XT47 | Q9XT47 macropus eu |
| 43 | 120.5 | 7.2 | 217 | 6 Q9BEC1 | Q9BEC1 bradyopus tr |
| 44 | 120.5 | 7.2 | 217 | 6 Q9BEC0 | Q9BEC0 cyclops dl |
| 45 | 120 | 7.1 | 260 | 11 Q9Z2V2 | Q9Z2V2 ratu mus norv |

ALIGNMENTS

RESULT 1
ID Q96Q17 PRELIMINARY; PRT; 270 AA.
AC Q96Q17;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HRANKL 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda T., Kuroyama H., Hirokawa K.;
RT "Human RANKL Isoform";
DR EMBL: AB061227; BAB71768.1; to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 270 AA; 30522 MW; 5C7754CE32E6F368 CRC64;

Query Match 84.4%; Score 1422; DB 4; Length 270;
Best Local Similarity: 100.0%; Pred. No. 1; le-121;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 MFALLGLGLGQVVCVALFFFRRAQMDPNRISEDTGHCIVRIILRLHENAEDPDTTLESQ 107
DB 1 MFALLGLGLGQVVCVALFFFRRAQMDPNRISEDTGHCIVRIILRLHENAEDPDTTLESQ 60
QY 108 DTKLIPDSGRIRKQAFQAVOKELQIHVSGHRAEKAWVDSWIDLAKRSKLEQAPFAH 167
DB 61 DTKLIPDSGRIRKQAFQAVOKELQIHVSGHRAEKAWVDSWIDLAKRSKLEQAPFAH 120
QY 168 LITNATDIPSGSHKVSLSWYHRCWAKISNMTFSNGKLIYQDGFYLLYANICFRHHET 227
DB 121 LITNATDIPSGSHKVSLSWYHRCWAKISNMTFSNGKLIYQDGFYLLYANICFRHHET 180
QY 228 SGLPATEYQLWVYTKTSIKIPSSHTLMKGSSTYVSGNSFHHYSINVGCFPLKSGE 287
|||||

| | | | | | |
|----|--|---|--------------|---------|---------|
| | RESULT | 3 | | PRT: | 318 AA. |
| ID | O9ESE2 | | PRELIMINARY; | | |
| AC | O9ESE2 | | | | |
| Dt | 01-MAR-2001 | (TREMBLrel. 16, Created) | | | |
| Dt | 01-MAR-2001 | (TREMBLrel. 16, Last sequence update) | | | |
| Dt | 01-DEC-2001 | (TREMBLrel. 19, Last annotation update) | | | |
| DE | RECEPTOR ACTIVATOR OF NF-KB LIGAND. | | | | |
| OS | Rattus norvegicus (Rat). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus. | | | | |
| OX | NCBI_Taxid=10116; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20540945; PubMed=11092398; | | | | |
| RA | Xu J.-K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
Zheng M.H. ; | | | | |
| RT | "Cloning, sequence and functional characterization of the rat
homologue of receptor activator of NF-kB ligand." | | | | |
| RL | J. Bone Miner. Res. 15:2178-2186(2000). | | | | |
| DR | EMBL; AF187319; AAGT7031.1; -- | | | | |
| DR | HSSP; P50591; 1DQG. | | | | |
| DR | InterPro: IPR003263; TNF_5. | | | | |
| DR | Interpro: IPR004478; TNF_family. | | | | |
| DR | Pfam: PF00229; TNF_1. | | | | |
| DR | PRODOM: PD008600; TNF_5; 1. | | | | |
| DR | SMART; SM00207; TNF_1. | | | | |
| DR | PROSITE; PS50049; TNF_2; 1. | | | | |
| SQ | SEQUENCE 318 AA; 35370 MW; 4B87AAD706AD098F CRC64; | | | | |
| | Query Match | 82.9%; Score 1396.5; DB 11; Length 318; | | | |
| | Best Local Similarity | 82.4%; Pred No.3e-119; | | | |
| | Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps | | | | |
| QY | 1 MRASRDYTEYLNGSEMGGGGPGAPHEGPLH APPPAZHOPPASRSMPVALLGLQLQ 59 | | | | |
| DB | 1 MRANNDYGKLINGSEMGSCEPVHGEPHLHPASPAPAAPPASRMFFALLGILGIQQ 60 | | | | |
| QY | 60 VVCVALFEPPFRAMDPNRISDGTHCIYRIILLHENAFODPTLSOPTKIIPDCSRR1 119 | | | | |
| DB | 61 VVICIALEFLFERAOMPENRISEDSTCFYRLIKLRNTGTLDSTLESDETALPDSCRMM 120 | | | | |
| QY | 120 KAFPFGAVOKEELHIIVSGSHIRAEKMAMDSDWLDAKRSLKEAOFAHLTINATIDPSGS 179 | | | | |
| DB | 121 KAFOGAVOEELCHIIHVPORFESGVPMAMEGSWILDVARRGKPEAPOAHLLTNADIPIGS 180 | | | | |
| QY | 180 HKVSLSSMYHDRGMAKITSMTFSNGKLITVNODGFYYLIYANICCRHNHTSGDLATEVLQM 239 | | | | |
| DB | 181 HKVSLSSMYHDGRGAKITSNNTLNSGKLRYNQDDGYFYLYANICFRHHETSSGVADYIQLM 240 | | | | |
| QY | 240 YYVKTKSIKKLPSSHTLMKGSGTYKWSCNSEPHFYTSINWGGEFKLRSGETSIEVSNPSSL 299 | | | | |
| DB | 241 YVVVKTISKIKIPPSSNNLMKGSGTYKWSCNSEPFHYTSINVGGEFKLRAGEELSIVOYNPSLT 300 | | | | |
| QY | 300 DPDODATYFGAFKYVDID 317 | | | | |
| DB | 301 DPDGDATYFGAFKYVID 318 | | | | |
| | RESULT 4 | | | | |
| ID | O9JJK9 | PRELIMINARY; | PRT; | 287 AA. | |
| AC | O9JJK9; | | | | |
| Dt | 01-OCT-2000 | (TREMBLrel. 15, Created) | | | |
| Dt | 01-OCT-2000 | (TREMBLrel. 15, last sequence update) | | | |
| Dt | 01-DEC-2001 | (TREMBLrel. 19, last annotation update) | | | |
| DE | RECEPTOR ACTIVATOR OF NF-KB LIGAND 2. | | | | |
| GZ | TNFSF1 OR RANKL 2. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Euthera; Rodentia; Sciuognathl; Muridae; Mus. | | | | |
| OX | NCBI_Taxid=10090; | | | | |

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21150053; PubMed-11250921;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of Three Isoforms of the Receptor Activator of Nuclear
 RT Factor-kappaB Ligand and Their Differential Expression in Bone and
 RT Thymus."
 RL Endocrinology 142:1419-1426(2001).
 DR EMBL: AB032771; BAA97257.1; -
 DR HSSP: P50591; 1D0G.
 DR MGD: MGI:1100089; Tnfef11.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR SEQUENCE 287 AA; 32234 MW; 8B2CE8EAC7B534CC CRC64;

Query Match 75.4%; Score 1271; DB 11; Length 287;
 Best Local Similarity 77.3%; Pred. No. 7.4e-108;
 Matches 245; Conservative 16; Mismatches 26; Indels 30; Gaps 2;

QY 1 MRASRDYTYLRGSEEMGGPGAPHEGRLHAPPPAPHPAPASRMFVALLGLGLGV 60
 DB 1 MRASRDYTYLR-----TRASRMFLALLGLGLGV 32
 QY 61 VCSYALFFYRAQMDPNRISEDTGTCIYRLRLHENADEFDTTLESODTKLIPDSRRIK 120
 DB 33 VCSIALFLYFRAQMDPNRISEDTGTCIYRLRLHENADEFDTTLESODTKLIPDSRRIK 90
 QY 121 QAFGGAQVQKELOHIVGSOHRAEKAMVDGSMIDLAKRSKLEAOPAHLTINATDIPSGH 180
 DB 91 QAFGGAQVQKELOHIVGSOHRAEKAMVDGSMIDLAKRSKLEAOPAHLTINATDIPSGH 150
 QY 181 KVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 240
 DB 151 KVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 210
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLD 300
 DB 211 YVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLD 270
 QY 301 PPDQATYFGAFKVDID 317
 DB 271 PPDQATYFGAFKVDID 287

RESULT 5
 Q9JUK8 PRELIMINARY; PRT; 199 AA.
 ID Q9JUK8
 AC Q9JUK8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
 GN TNFSF11 OR RANKL 3
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21150053; PubMed-11250921;
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
 RT "Determination of Three Isoforms of the Receptor Activator of Nuclear
 RT Factor-kappaB Ligand and Their Differential Expression in Bone and
 RT Thymus."
 RL Endocrinology 142:1419-1426(2001).
 DR EMBL: AB032772; BAA97258.1; -

DR HSSP: P50591; 1D0G.
 DR MGD: MGI:1100089; Tnfef11.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR SEQUENCE 199 AA; 22150 MW; 401C13EB58CE16 CRC64;

Query Match 53.9%; Score 909; DB 11; Length 199;
 Best Local Similarity 85.4%; Pred. No. 4.8e-75;
 Matches 170; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 119 IKAQGAQVQKELOHIVGSOHRAEKAMVDGSMIDLAKRSKLEAOPAHLTINATDIPSG 178
 DB 1 MKQAFGGAQVQKELOHIVGPORFSGAPAMEGSMIDLVAQRKPEAOPAHLTINATDIPSG 60
 QY 179 SHKVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 238
 DB 61 SHKVSLSWYHNRGMAKISNMTFSNGKLIYNODGFYLLANICFRHHETSGDLATEYLQ 120
 QY 239 MYYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLD 298
 DB 121 MYYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLD 180
 QY 299 LDPDQATYFGAFKVDID 317
 DB 181 LDPDQATYFGAFKVDID 199

RESULT 6
 Q91ZT9 PRELIMINARY; PRT; 53 AA.
 ID Q91ZT9
 AC Q91ZT9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE TNFSF11 (FRAGMENT).
 GN TNFSF11.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F344;
 RA Odgren P.R., Kim N., van Wesenbeeck L., Mackay C.A., Mason-Savay A.,
 RA Safadi F.F., Popoff S.N., Lengner C., van Hul W., Choi Y., Marks S.C.;
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
 RT the tnfrsf11 (TNFR, RANKL, ODF, OPEL) gene."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF425669; AAL23963.1; -
 FT NON_TER 1
 FT SEQUENCE 53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;

Query Match 15.5%; Score 262; DB 11; Length 53;
 Best Local Similarity 90.6%; Pred. No. 8.3e-17;
 Matches 48; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 265 SGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLDPPDQATYFGAFKVDID 317
 DB 1 SGNSEFHYFSINVGFEFLRAGEEISIEVSNPSLLDPPDQATYFGAFKVDID 53
 RESULT 7
 Q9DDZ5 PRELIMINARY; PRT; 214 AA.
 ID Q9DDZ5
 AC Q9DDZ5;

RT "pig-tailed monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kiril V., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mullatta; STRAIN=RHEBUS MONKEY;
RA Kiril V., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB035140; BAA90296.1; -
DR EMBL: AB035138; BAA90294.1; -
DR EMBL: AB035139; BAA90295.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR003263; TNE_5.
DR InterPro: IPR003636; TNE_abc.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE_1.
DR PRINTS: PR01234; TNECROSISCT.
DR ProDom: PD002012; TNE_abc; 1.
DR ProDom: PD008600; TNE_5; 1.
DR SMART: SM00207; TNE_1.
DR PROSITE: PS00251; TNE_1; 1.
DR PROSITE: PS50049; TNE_2; 1.
SQ SEQUENCE 280 AA; 31367 MM; F0B284D61A132EB4 CRC64;

Query Match 11.0%; Score 186; DB 6; Length 280;
Best Local Similarity 22.1%; Pred. No. 7.4e-09;
Matches 69; Conservative 44; Mismatches 103; Indels 96; Gaps 11;

QY 22 PGAPHEGPLHAAPPAP-----HPPAASRS-----MFVALTGLTGVVCS 63
DB 45 PPPPPPPPLPPPPSPPLPLPLPKKRGNSTGLCLVMFVVALVGLGLG----- 99
QY 64 VALFFEFRAQMDPNRISEDTGHCYRILRLHENADPDTTLESQTKLIPDSCRIRKQAF 123
DB 100 --MFOLFHLQ-----KELAELESTSQKHTA----- 123
QY 124 QGAVQKELQHTVSSQHIRAEKAMVDGSWDLAKRSKLEAPFAHLT--INATDIPSGSHK 181
DB 124 --SLEKQIGH-----PSPPEKKEQRKVAHLTGKPNRSM----- 158
QY 182 VSLSSWYHDGMAKISNMTFSNGKLIVNODGFYUVAANICFRHHETSGDLATEYLQIMVY 241
DB 159 ---LEWEDTYGIVLLSGVAKKGGVYINETGLYFYVSKYVFR---GQSCFN-LPLSHK 209
QY 242 VYKTSIKIPSSHTLMKGGSTKYSNGSEFHFYSINVGCFKLSRGEISIEVSNPSLDP 301
DB 210 VYMRNSKYPQDLYVMEKMMSYCT--TGQWMAHSSYLGAVFNLTSADHLVYVNSLSLVNF 268
QY 302 DODATYFGAFKV 313
DB 269 EESQTFEGLYKL 280

RESULT 13
Q9BDM5 PRELIMINARY: PRT; 280 AA.
AC Q9BDM5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;

RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-2183618; PubMed-11491535;
RX Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL: AF344856; AKK37539.1; -
DR HSSP: P01375; 4TSV.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR003263; TNE_5.
DR InterPro: IPR003636; TNE_abc.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE_1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PRINTS: PR01234; TNECROSISCT.
DR ProDom: PD002012; TNE_abc; 1.
DR ProDom: PD008600; TNE_5; 1.
DR SMART: SM00207; TNE_1.
DR PROSITE: PS00251; TNE_1; 1.
DR PROSITE: PS50049; TNE_2; 1.
SQ SEQUENCE 280 AA; 31377 MM; 729EA61436F2D398 CRC64;

Query Match 10.9%; Score 184.5; DB 6; Length 280;
Best Local Similarity 22.4%; Pred. No. 1e-08;
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGPLHAAPPAPHPP-----AASRS-----MFVALTGLTGVVCS 62
DB 46 PPPPPPPPL--PPPPPLPLPLPLPKKRGNSTGLCLVMFVVALVGLGLG----- 99
QY 63 SVALFFEFRAQMDPNRISEDTGHCYRILRLHENADPDTTLESQTKLIPDSCRIRKQA 122
DB 100 --MFOLFHLQ-----KELAELESTSQKHTA----- 123
QY 123 FQGAVQKELQHTVSSQHIRAEKAMVDGSWDLAKRSKLEAPFAHLT--INATDIPSGSH 180
DB 124 --SLEKQIGH-----PSPPEKKEQRKVAHLTGKPNRSM----- 158
QY 181 KVSLSWYHDGMAKISNMTFSNGKLIVNODGFYUVAANICFRHHETSGDLATEYLQIMV 240
DB 159 ---LEWEDTYGIVLLSGVAKKGGVYINETGLYFYVSKYVFR---GQSCFN-LPLSH 208
QY 241 VYKTSIKIPSSHTLMKGGSTKYSNGSEFHFYSINVGCFKLSRGEISIEVSNPSLDP 300
DB 209 KYVMNSKYPQDLYVMEKMMSYCT--TGQWMAHSSYLGAVFNLTSADHLVYVNSLSLVN 267
QY 301 PDODATYFGAFKV 313
DB 268 FEESQTFEGLYKL 280

RESULT 14
Q9BDN1 PRELIMINARY: PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD95L PROTEIN.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383618; PubMed-11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;

"Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344847; AAK37606.1; -
 DR HSSP: P01375; 4TSV.
 DR InterPro: IPR002965; P-rich_extensn.
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR003636; TNF_5.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 280 AA; 31407 MW; 729BA60067B7D398 CRC64;

Query Match 10.8%; Score 182.5; DB 6; Length 280;
 Best Local Similarity 22.4%; Pred. No. 1.5e-08;
 Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;
 QY 22 PGAPHGPIHAPPPAPHPQPP-----AASRS-----MFVALLGLGQVVC 62
 DB 46 PPPPPPPPL-PPPPPPPLPLPLPKRGHNSGLCLLNFVNLVGLGLG---- 99
 QY 63 SVALFFYFRAQMDPNRISDGTICIRILRLHFNADFODTLESQDTLIPSCRRIKQA 122
 DB 100 ---MFQLFHLQ-----KELAEIRSTGSKHTA----- 123
 QY 123 FQCAVQKELQHYVSGHIAEKAMVDGSLDLAKRSKLEAOPPAHLT--INATDIPSGSH 180
 DB 124 ---SSEKQIGH-----PSPPEPKKEQKRVVHLTGKPNRSMP---- 158
 QY 181 KVISLSMYHNRGMAKISNMTFNGKLIYNQDGFYLYANICRHHETSGLATEYLQLMV 240
 DB 159 ----LEMEPTYGIVLLSGYKVKKGLVINETGLFYYSKYVFR-----GQSCFN-LPLSH 208
 QY 241 VYTKTSIKIPSSHLLMKGSGSTYWGSEFNHYSTINVGGEFKLRSGEISIEVSNPSLID 300
 DB 209 KYVMRNSKYPQDLVMEGKMMSYCT-TGQMAHSSVYLGAVFNLSTDHLYVVSSELSLVN 267
 QY 301 PQDQATYFGAFKV 313
 DB 268 FEESQTFEGLYKL 280

RESULT 15
 Q9BDN3 PRELIMINARY; PRT; 261 AA.
 AC Q9BDN3; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CD154 PROTEIN.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
 NX NCBI_TaxID=9483;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344844; AAK37603.1; -
 DR HSSP: P29865; 1ALY
 DR InterPro: IPR003263; TNF_5.
 DR InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF_1.
 DR ProDom: PD008600; TNF_5; 1.
 DR SMART: SM00207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 SQ SEQUENCE 261 AA; 29360 MW; 10CA580923754EB CRC64;

Query Match 10.1%; Score 169.5; DB 6; Length 261;
 Best Local Similarity 24.6%; Pred. No. 2.1e-07;
 Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;
 QY 33 PPPPAPHPPASRSMFVALLGLG-IGVVCVAFYFPPRQMDPNRISDGTICIRIL 91
 DB 8 PVPKSAATGPPVSMKIFMLILFVLITOMIGSALFAVYLHRLD--KIEDE-----R 57
 QY 92 RLHNADFQDT--TLESQDTKLIPDCRRIKQAQFQCAVQKELQHYVSGHIAEKAMVDG 149
 DB 58 NLHEDFVFNMKTITQRCNTGERSLSLNCCEIKSQFEGV-KDIM-----LNKEKKEN 109
 QY 150 SWLDLAKRSKLEAOPFAHLTINATDIPSGSHKVISLSWYHNRGMAKISN--MTFSNCK-L 206
 DB 110 SF-EMQKGDQ-NPQIAAHVISEA-----SKTTSVLQW-AEKGYTMSNNLVTLQNGKOL 161
 QY 207 IVNQDGFYLYANICFRHHETSGLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTIKY 264
 DB 162 TYKRGGLYIYAQVYFCCNREASSAP-----FISLCLKPPRRERILLRANH-- 212
 QY 265 SGNSEFNHYSTINVGGEFKLRSGEISIEVSNPSLIDPQDQATYFGAFKV 313
 DB 213 SSAPKPGQGSIHILGIGIFELQPGASVYFVNTDPSQVSHQGTFTSGLLKL 261

Search completed: July 8, 2002, 19:52:38
 Job time: 12582 sec

Tue Jul 9 13:21:07 2002

us-09-865-363-13.rspt

Page 8